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Post-processing: Minimum Match 0%
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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| cacterization, | The new kallikrein-like gene, KLK-L2. Molecular characterization, | TITLE |
| | Yousef, G.M. and Diamandis, E.P. | AUTHORS |
| | 1 (bases 1 to 11570) | REFERENCE |
| Homo. | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | |
| Euteleostomi; | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| | Homo sapiens | ORGANISM |
| | Homo sapiens (human) | SOURCE |
| | | KEYWORDS |
| | AF135028.1 GI:4589282 | VERSION |
| | AF135028 | ACCESSION |
| complete cds. | Homo sapiens kallikrein-like protein 2 KLK-L2 gene, complete cds. | DEFINITION |
| PRI 27-JUN-2000 | AF135028 11570 bp DNA linear | LOCUS |
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Pred. No. is the number of results predicted by chance to have

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/translation="MATARPPMMWVLCALITALLLGVTEHVLANNDVSCDHPSNTVPS
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/product="kallikrein-like protein:
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                                                                         Direct Submission
Submitted (01-JUL-2002) DOE Joint Genome Institute, 2800 M
Drive, Walnut Creek, CA 94598, USA
On Jul 1, 2002 this sequence version replaced gi:14971176.
Draft Sequence Produced by DOE Joint Genome Institute
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.6% of Sequence;
Estimated Total Number of Errors is 0.6.
NOTE: Shatter libraries failed to resolve dinucleotide repeat.
                                                                                                                                            DOE
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Submitted (07-OCT-1999) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
3 (bases 1 to 107487)
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AC011483.7 GI:21637461
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Mammalia; Eutheria; Primates;
1 (bases 1 to 107487)
DOE Joint Genome Institute and
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                                                      www.jgi.doe.gov
Finishing Completed at Stanford Human Genome
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="19"
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| TRGTCCCAGAAATNAACTGAGAAG 2071 | <pre>/note="serine protease" /codon_start=1 /product="ACO protease"</pre> | | CTCTCTAGTTGAACCCTGGGAACAATTTCCAAAACTGTCCAGGGCGGGGGGTTGCGTCTCA |

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GLVSFGKAPCGQVGVPGVYTNLCKFTEWIEKTVQAS"
complement(<131301. .>140303)
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QAALVMENELFCSGYLVHPQWVLSAAHCFQNSYTIGLGLHSLEADQEPGSQMYEASLS
VRHPEYNRPLLANDLMLIKLDESVSESDTIRSISIASQCPTAGNSCLYSGWGLLANGR
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complement(join(<94602. .94754,96027. .96163,96247. .96497
96919. .97081,98345. .>98405))
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RGRAVGGGVLVHPQWVLTAAHCIRNKSVILLGRHSLEHPEDTGQVFQVSHSEFHELYI
MSLLKNRFLRFQDDSSHDLMLLRLSEPAELTDAVKVWDLPTQEPALGTTCYASGWSI
EPEEFLTPKKLQCVDLHVISNDVCAQVHPQKVTKFMLCAGRWTGGKSTCSGDSGGPLV
                                                                                                                                                                                                                        complement(join(<131301. .131456,136310.
136529. .136785,137525. .137690,140255.</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96919. .97081,98345. .98405))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="serine protease"
complement(join(94602...94)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="GI:11244761"
/translation="MMDLVLSLALSVGCTGAVPLIQSRIVGGWECEKHSQPWQVAVYS
/translation="MMDLVLSLALSVGCTGAVPLIQSRIVGGWECEKHSQPWQVAVYS
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MSLLKHQSLRPDEDSSHDLMLLRLSEPAKITDVVKVLGLPTQEPALGTTCYASGWGSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNGVLQGITSWGSEPCALPERPSLYTKVVHYRKWIKDTIVANP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TUTANS LATÉON="NWILLITLSFILASTAAQDGDKLLEGDECAPHSQPWQVALYERGR
FNCGASLISPHWYLSAAHCQSBFMRVRLGEHNURKRDGFEQLETTSRVLIPHPRYEARS
HRNDIMILIALVQPARLINGVURPAVLPTRCPHGEACYVSGWGLVPLSSBYSLDDTILG
ANISIISDTSCDKSYPGRLTNTMVCAGAEGRGAESCEGDSGGPLVCGGILQGIVSWGD
     /product="stratum corneum trypsin-likė serine protease"
/protein_id="AAG33358.1"
/db_xref="GI:11244763"
                                                                                                                       /gene="KLK5"
/note="synonym: SCTE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="serine protease"
/protein_id="AAG33357.1"
/db_xref="GI:11244762"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPEEFLRPRSLQCVSLHLLSNDMCARAYSEKVTEFMLCAGLWTGGKDTCGGDSGGPLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="glandular kallikrein"
join(61139. .61184,62391. .6255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="prostate specific antigen"
/protein_id="AAG33355.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="KLK3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VPCDNTTKPGVYTKVCHYLEWIRETMKRN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAG33354.1"
/db_xref="GI:11244759"
                                                                                                                                                                                                   /gene="KLK5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="glandular kallikrein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="KLK2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          )oin(<61139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="KLK2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="serine protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="prostate
join(42595. .42640,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         )oin(<42595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="KLK3"
                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAG33356.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="KLK2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="GI:11244760"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="KLK3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="serine protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .47769)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .>47769)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66229)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .>47769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .42640,43880.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .61184,62391. .62550,64142. .64428,64542. .64678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .61184,62391. .62550,64142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .42640,43880. .44039,45669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specific antigen",43880. .44039,45669. .45955,46099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .94754,96027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .96163,96247. .96497
                                                                                                                                                                                                                        .>140303))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .64428,64542. .64678,
                                                                                                                                                                                                                                                 .136443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .45955,46099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .46235
Best Local Similarity
                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
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                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="KLK7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="KLK7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="KLK7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MWVLCALITALLLGVTDARSDDSSSRIINGSDCDMHTQPWQAAL"
  100.0%;
  Score 2071;
Pred. No. 0
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complement(join(183943. .184098,185635. .185768, 187865. .188127,188293. .188452,188967. .189036)
//note-"serine protease; also called ovasin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="stratum corneum chymotryptic enzyme"
complement(join(165420. .165575,167672. .167808,
168124. .168371,169651. .169798,170211. .170283))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="synonym: SCCE"
complement(join(<165420.
168124...168371,169651...
                                                           /translation-"MKLGLLCALLSLLAGHGWADTRAIGAEECRPNSQPWQAGLFHLT
RLFCGATLISDRWLLTAAHCRKPYLWVRLGEHHLWKWEGPEQLFRVTDFFPHPGFNKD
LSANDHNDDIMLIRLPRQARLSPAVQPLNLSQTCVSPGMQCLISGWGAVSSPKALFPV
                                                                                                                                                                                                                                                                                             complement(join(190980. .191129,191573. 194324. .194589,197048. .197204,197370. /note="scrine protease"
                                                                                                                                                                                                                                                                                                                                                                                                   DGALQGITSWGSDPCGRSDKPGVYTNICRYLDWIKKIIGSKG"
complement(join(<190980. 191129,191573. 1;
194324. 194589,197048. 197204,197370. .>15
/product="kallikrein-like 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PWQAALFQGQQLLCGGVLVGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQ
SIPHPCYNSSDVEDHNHDLMLLQLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(<183943. .184098,185635.
187865. .188127,188293. .188452,188967.</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYSTQTHVNDLMLVKLNSQARLSSMYKKVRLPSRCEPPGTTCTVSGWGTTTSPDVTFP
SDLMCVDVKLISPQDCTKVYKDLLENSMLCAGIPDSKKNACNGDSGGPLVCRGTLQGL
VSWGTFPCGQPNDPGVYTQVCKFTKWINDTMKKHR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(146834. .146986,149628. .149764, 151186. .151433,155052. .155208,155948. .155987),note="serine protease; also called neurosin or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(<146834...146986,149628.
151186...151433,155052...155208,155948.</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGYSHPGHSNDLMLIKLNRRIRPTKDYRPINVSSHCPSAGTKCLYSGWGTTKSPQVHF
PKVLQCLNISYLSQKRCEDAYPRQIDDTMFCAGDKAGRDSCQGDSGGPVVCNGSLQGL
VSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS"
TLQCANISILENKLCHWAYPGHISDSMLCAGLWEGGRGSCQGDSGGPLVCNGTLAGVV
SGGAEPCSRPRRPAVYTSVCHYLDWIQEIMEN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="neuropsin"
/protein_id="AAG33361.1"
/db_xref="GI:11244766"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VALLSGNQLHCGGVLVNERWVLTAAHCKMNEYTVHLGSDTLGDRRAQRIKASKSFRHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="stratum corneum chymotryptic enzyme"
/protein_id="AAG33360.1"
/db_xref="GI:11244765"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLVSREECEHAYPGQITQNMLCAGDEKYGKDSCQGDSGGPLVCGDHLRGLVSWGNIPC
GSKEKPGVYTNVCRYTNWIQKTIQAK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSPRENFPDTLNCAEVKIFPQKKCEDAYPGQITDGMVCAGSSKGADTCQGDSGGPLVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(<165420. .>170283)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="protease M"
/protein_id="AAG33359.1"
/db_xref="GI:11244764"
                                                                                                                                                                  /protein_id="AAG33362.1"
/db_xref="GI:11244767"
                                                                                                                                                                                                                                    /product="kallikrein-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQ"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="neuropsin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MARSLLLPLQILLLSLALETAGEEAQGDKIIDGAPCARGSHPWQ/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLCGGVLIHPLWVLTAAHCKKPNLQVFLGKHNLRQRESSQEQSSVVRAVIHPDYDAAS
HDQDIMLLRLARPAKLSELIQPLPLERDCSANTTSCHILGWGKTADGDFPDTIQCAYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MKKLMVVLSLIAAAWAEEQNKLVHGGPCDKTSHPYQAALYTSGH/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="protease M"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLSPVYESGQQMFQGVKSIPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .165575,167672. .167808, .169798,170211. .>170283))
                                                                                                                                                                                                                                    Ψ
                                                                                                                                                                                                                                                                                                                                    .191709,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .155987))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .149764,
.>155987))
                                                                                                                                                                                                                                                                                                                                                                                                                                          .>197412))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .189036))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .>189036))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .191709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .185768
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DB 9;

Length 230000;

| B 64 | Оy | D Qy | р, _Q | Db. Qy | QУ | Db Qy | Оy | Qy Db | р. 9 | 0y 0 | P Q | B 64 8 | 2 2 5 | 3 S | P 6 | F . S | Matc Oy | |
|---|---|---|--|--|---|--|--|--|--|---|---|---|---|---|--|---|---|---|
| 1021 AAGAGGAAGATGGAGTGACAAATGGGGTTTAAAGGTTGAACTTGGAGGCCAGG 1080 | | 901 GGCGGAGAGATACACGATGAGGGAGACAGGCTGGAACAGAAAGTAGAGACGAAGATTCGA 960 | 841 GTGTCCAGTAAGAGAAATAAGGCCTGCACAGGCTGGAGGGGAGAGTGAGAGAGA | 781 CGTATTTTTGCAGAAGGGAGGTATAAGGATGGGTTGGTGGAGAATGGGGAAGGTGT 840 | 721 ATCCAGCTTCAGATGCCCACAGTGCCCAGATCGAGGAACCCTCATCCAGGGGCTGAGAAAC 780 | 661 TGCCAAGTGTGCTGTTCAACATGCTATGATGCACACGGCAGGCCTCCACAACAACCATT 720 | 601 GGAGACATTTTTGGTTGTCACAACTATATGGAGGGGCATTACTGGCAACTAATGGATAGA 660 | 541 TCCAAGCGAATGGATTTCTATTGGGAGTGATTCTGCCCCTAGAAGACACTGGCAATACCA 600 | 481 | 421 GAGGAAGGAAGGAAAGAAGAAGAAGAAGAAAAAAATGACTGTTGAAGAGCAGTGAGTAT 480 | 361 GAAAGAAAGGAAGAAAGAAAGAAAGAAAAGAAAGAAAG | 301 AAAGGAAGGAAGGAGAGAAGAAAGAAAGGAAGGAAGGA | 241 CARAGCAAGACGTTTTTGTCAGAAAGAAAAAAAAAAAAGAGACGAAGGAGGAGGAGGAG | 181 CGTTTGAGGCTGCGGTAAGCCATGACTGCAGCACTGCAGACAGCAGCCTGGGTGA 240 | 121 CTTGCACCTGTAGTTCCAGCTACTTGGGAGGCTGAGGTGGGAGAATTGCTTGAGCCCAAA 180 111 | 120 TAAAAGAGATAGATAAATATGTAAATAAATAAAAAAAAA | Matches 2071; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 AAACAGACCAAAAACTTCCTGCCGCGGGGCCTCATGTTCCCCAAGTGGAAGACAGGCAA 60 | |
| RESULT 4 AC027602/ LOCUS | Ωy Db 13 | L | ь | ь | – | <u>.</u> | – | 0v 13 | _ | Qу рь 13 | Qy Db 13 | ш | Qу ДЬ . 13 | Qy Db 13 | 13 | Qy Db 13 | Qy Db . 13 | |
| /c AC027602 | 10 | 668 | 28 | 88 5 | 48 | 1/41 ACTCCTGAG | 68 | 428 | 1561 GCCTCTCTC | | 8 1 | · 80 1- | 1321 GCGCTCCAA 31728 GCGCTCCAA | 1261 GGCAGGAGA 31788 GGCAGGAGA | 8 1 | 1141 GGCCAGGAG 31908 GGCCAGGAG | 1081 CATGGTGGC 31968 CATGGTGGC | |
| 217 | 41 CCAAATTTAGTCCCAGAAATAAACTGAGAAG 2071 | ATCTCCCTGGGGGACTTTCATCCTCAAGCTCAAGGCCCATCCCTTCTCTCTGCAGCTCTGACATCCCTGAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGAC | CTCTCTAGTTGAACCCTGGGAACAATTTCCAAAACTGTCCAGGGGGGTTGCGTCTCAGGGCGGGGTTGCGTCTCAAAACTGTCCAAGGGCGGGGTTGCGTCTCAAAACTGTCCAAGGGCGGGGGTTGCGTCTCAAAACTGTCCAAGGGCGGGGGTTGCGTCTCAAAACTGTCCAAGGGCGGGGGTTGCGAACAATTTCCAAAAACTGTCCAAGGGCGGGGTTGCGTCTCA | CCCCTGACCCCATGTCTCCTGGACTCAGGGTCTGCTTCCCCCACATGGGCTGACCGTGTCCCACGTGTCTCA | | ACICCIONALICA CONSANCIANO CONCENCIO CONTROLO CARRECA CONTROLO CONTROLO CONTROLO CONTROLO CONTROLO CONTROLO CONT | | | GCCTCTCATGCCCCCCTTTCTCTCCTGCAGGCTGATTCTGGGGGGCCCYGTGGYCTGCAGGCCCTGTGGAGGCCCAGGCTGATTCTGGGGGGGCCCAGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGGGG | TCATCTATGGCATCTCTGGGTCTCTCATGTCTCTCTGCCACTTTGCCACATCTCT | TTTTCTGCATTTCTTCATCTCTGTACTTTCCATCTCTGTGTGTCTGTTCCCATCTGCTTC TTTTCTGCATTTCTTCATCTCTGTACTTTCCATCTCTGTGTGTG | AGTGAAATATTAATAACATTCTCCCTCTCTCTCTCTTTTGCCTCTCTCT | GCGCTCCAACCTGGGCAACAGAGTAAGACTCCATCTCAAAAAAAA | GCAGGAGAATTGCTTGAACCCGGGAGATGGAGGCTGCAGTGAGCTGAGGTCAGGCCACT | ACAAAAATTAGCCGGGTGTGGTGATGGACACCTGTAGTCACACACTACTTGGGAGGCTGA | GGCCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCTACAAAAAAAT | CATGGTGGCTCACGCCTGTAATCCCAACACTTTGGAGGCTGAGGTGGGCGAATCACTTGA 1140 | |
| 346 bp 1 | CTGAGAAG CTGAGAAG 1: | TCAAGCTCAGO | ATTTCCAAA | TCAGGGTCTC | CCTTCCCAG | AGCACACCGGC | AGTTCACCAL | CCTGGGGAGA | TCCTGGGAGA | TCTCATGTCT | ACTITCATO | CTCTCTCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC | PAAGACTCCAT | GAGATGGAGG | ATGGACACCT | GCCAACATGG GCCAACATGG | CAACACTTTG CAACACTTTG | |
| DNA line | 130978 | GCCCATCCCT | ACTGTCCAGGG | CTTCCCCAC | GATGTTGAGA | ATCCCCACCT | TITITITITI | TITITITI | TTACCCTTGT | CCTTCTGCCC | TCTGTGTGTC | TTTTGCCTGT | CTCAAAAAAA CTCAAAAAAAA | CTGCAGTGAG CTGCAGTGAGC | GTAGTCACAGO | TGAAACCCCG5 TGAAACCCCG5 | GAGGCTGAGGI BAGGCTGAGGI | |
| ar HTG | | TCTCTGCAGCT | | ATTGGGCTGAC | ATGTTCATCTC | | | | GGGCCTGTGGT | ACTTTGCCACA | TGTTCCCATCT | GTCTCCATCTC | AAAAAGCTGGA \$AAAAGCTGGA | CTGAGGTCAGG | CTACTTGGGAG | TCTCTACAAAA CTCTACAAAA | rgggcgaatca rgggcgaatca | • |
| 24-AUG-2002 | • | | TCTCA 131069 | | TCCAG 131189 | | | | CTGCA 1520 CTGCA 131429 CAGAC 1680 | | | TGTCT 1440 TGTCT 131609 | | CCACT 1320 CCACT 131729 | GCTGA 1260 GCTGA 131789 | | CTTGA 1140 CTTGA 131909 | |
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-AUG-2002) white the following the street, Cambridge, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA 2007 15 2000 this sequence version replaced gi:11136831
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AC027602
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Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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                                                                                                                                                                                                                                                                           http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zimmer,A. and Zody,M.
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                                                                                                                                                                                                                                                                                                                      Nov 15, 2000 this sequence version replaced repeats were identified using RepeatMasker. t. A.F.A. & Green, P. (1996-1997)
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Contact: sequence_submissions@genome.wi.mit.edu
                                                                                               Web site: http://www-seq.wi.mit.edu
                                                                                                                                                    Center code: WIBR
                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (24-AUG-2002) Whitehead Institute/MIT Center for Genome
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Eutheria; Primates;
                                                                                                                                                                                                                                     Genome Center
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                                                                                                                                                                                     for Genome Research
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NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert size: 194000; agarose-fp
Insert size: 216246; sum-of-contigs
Quality coverage: 11.9 in Q20 bases; agarose-fp
Quality coverage: 10.7 in Q20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Consensus quality: 210748 bases at least Q40 Consensus quality: 213655 bases at least Q30 Consensus quality: 215058 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: M13; M77815; 31% of reads Sequencing vector: Plasmid; n/a; 69% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center clone name: 795_B_6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124575
134665
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8250
9593
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                                                                                                                                                                                                         9693. .10733
                                                                                                                                                                                                                                             8250.
                                                                                                                                                                                                                                                         vector_side:left"
                                                                                                                                                                                                                                                                                clone_end:SP6
                                                                                                                                                                     10834.
                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic
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                                                                                                              'note="assembly_fragment"
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                                                                                                                                                                                  /note="assembly_fragment"
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                                                                                                                                                                                                                                                                                           /note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                   /clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                        /clone="RP11-795B6"
                                                                                                                                                                                                                                                                                                                                                                                      /chromosome="19"
                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Summary Statistics
                                                                                                                                                                                                                     assembly_fragment"
                        .124474
                                                            .35434
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                                                                                                                                                                                                                                             9592
                                                                                                                                                                     .13519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of 8149 bp in length gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap of 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig of 46474 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conti
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gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g of 10090 bp in length
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| 1920 TCTCTCTAGTTCAACCCTGGGAACAATTTCCAAAACTGTCCAGGGGGGGG | Qy | Qy 841 GTGTCCAGTAAGAGAAATAAGGCCTGCACAGGCTGGAGGGGAGAGTGAGAGAGA | ٥ |
|---|----------------|--|------------|
| 63 GCCCCTGACCCCATGTCTCCTGGACTCAGGGTCTGCTTCCCCCCACATTGGGCTGACCGTG | Db x3 | Qy 781 CGTATTTTTGCAGAAGGGAGGTATAAGGATGGGTTGGTGGAGAATGGGGAAGGTAGT 840 | <u> </u> |
| | Db V | Oy 721 ATCCAGCTTCAGATGCCCACAGTGCCCAGAGTACCAGAGGAACCCTCATCCAGGGGCTGAGAAC 780 | g 0 |
| 1/40 AACTCCTGAGTCATCCCAGGACTCAGCACACCGCATCCCCACCTGCTGCAGGGACACCC 1/99 11/41 | Db Q | OY 661 TGCCAAGTGTGCTGTTCAACATGCTATGATGCACAGGCCAGGCCTCCACAACAACCATT 720 | g o |
| CCGGGTGTCTRCACGAACCTCTGCAAGTTCACCAAGTGGATCCAGGAAACCATCCAGGCC | g dg | OY 601 GGAGACATTTTTGGTTGTCACAACTATATGGAGGGGCATTACTGGCAACTAATGGATAGA 660 | g o |
| AATGGCTCCCTGCAGGGACTCGTGCCTGGGGAGATTACCCTTGTGCCCGGCCCAACAGA | Qy Db | OY 541 TCCAAGCGAATGGATTTCTATTGGGAGTGATTCTGCCCCTAGAAGACACTGGCAATACCA 600 | g o |
| TGCCTCTCATGCCCCCCTTTCTCTCTCTGCAGGGTGATTCTGGGGGGCCTGTGGTCTGC | Оу | 481 TATTATAGGAGGTAATTATAGGGAGGTATGGGGAAATTGAAGACAGGAAACACAAATTAG. 540 | g o |
| 1500 CTCCATCTATGGGCATCTCTGGGTCTCTCATGTCTCCTTCTGCCCACTTTGCCACATCTC 1559 | Оy | Qy 421 GAGGAAGGAAAGAAGGAAAAGAGGAAAAAAATGACTGTTGAAGAGCAGTGAGTAT 480 | g o |
| TTTTTCTGCAFTTCTTCATCTCTGTACTTTCCAFCTCTGTGTGTCTGTTTCCCATCTGCTTTTTTTCTGCAFTTCTTCATCTGTACTTTCCATCTGTGTCTGTGTCTTCCATCTGTGTTTCCATCTGTTTCCATCTGTTTTCTGTTTCCATCTGTTTCCATCTGTTTTCTGTTTCCATCTGTTTCTGTTTCTGTTTCCATCTGTTTTCTGTTTTCTGTTTTCTGTTTTCTGTTTTCTGTTTTCTGTTTTTT | Дb | Oy 361 GAAAGAAAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAG | g g |
| 380 GAGTGAAATATTAATAACAATCTCCCTCTCTCTCTCTTTGCCTGTGTCTCCATCTGTGTC | Оу | Oy 301 AAAGGAAGGAAGGAAGGAAAGGAAAGGAAAGAAAGGAAGGAAAGGAAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAAGGAAGGAAAGGAAGAAGAAAGAAAGAAAGAAAA | <u>p</u> 0 |
| GCGCTCCAACCTGGGCAACAGAGTAAGACTCCATCTC-AAAAAAAAAA | Оу | QY 241 CAAAGCAAGACGTTTTGTCAGAAAGAAAAAAAAAAAGAGAGGAGGAAGGA | g o |
| GCCAGGAGAATTGCTTGAACCCGGGAGATGGAGGCTGCAGTGAGGTGAGGTCAGGCCAGTGAGGCGAGGAGAATTGCTTGAACCTGGGAGATGGAGGCTGCAGTGAGCTGAGGCTCAGGCCACT | do Qy | OY 181 CGTTTGAGGCTGCGGTAAGCCATGACTGCACTGCTGCACTCCAGACAGCAGCCTGGGTGA 240 | <u> </u> |
| 201 | Db Qy | OY 121 CTTGCACCTGTAGTTCCAGCTACTTGGGAGGCTGAGGTGGGAGAATTGCTTGAGCCCAAA 180 | g ø |
| 141 GGCCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCCCGGTCTCTACAAAAAAAT | Оу | | g o |
| 1081 CATGGTGGCTCACGCCTGTAATCCCAACACTTTGGAGGCTGAGGTGGGCGAATCACTTGA 1140 | Db Oy | AAACTTCCTGCCGCGTGGACCTCATGTTCCCCAAGTGGAAGACAGGCAA 60 | g o |
| 1021 AAGAGGAAGATGGAGTGGAGAGTGACAAATGGGGTCTAAAGGTTGAACTTGGAGGCCAGG 1080 | Qу | Query Match 96.1%; Score 1990; DB 2; Length 217346; Best Local Similarity 98.7%; Pred. No. 0; Matches 2045; Conservative 0; Mismatches 5; Indels 22; Gaps 3; | |
| 961 GATGTGGAGAGGAAGGGTCACAGACCCCCCCGAAATGATGTGTGGACAACAGGAATCTGG 1020 | Qy Db | Clone_end:79 clone_end:70 clone | Ο¤ |
| 194083 GTGTCCAGTAAGAGAAATAAGGCCTGCACAGGCTGGAGGGAG | Qy Qy db | misc_feature 134755. 162343 /note="assembly_fragment" misc_feature 162444208917 /note="assembly_fragment" misc_feature 209018217346 /note="assembly_fragment" | |

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REFERENCE
AUTHORS
TITLE
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AC130782/c
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192883 CCCAAATTTAGTCCCAGAAATAAACTGAGAAG 192852
                                                                                                                                                                        The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8% average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2040 CCCAAATTTAGTCCCAGAAATAAACTGAGAAG 2071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1980 AATCTCCCTGGGGCACTTTCATCCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGA 2039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Benjamin, B., Blakesley, R. W., Bouffard, G.G., Brinkley, C., Brooks, S. Cariaga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S., L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J., Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schandler, K., Schouler, M.G., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L. Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D. MISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (22-NOV-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (14-AUG-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 200792)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Nov 22, 2002 this sequence version replaced gi:22218452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan troglodytes (chimpanzee)
Pan troglodytes
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Pan troglodytes clone CH251-355A20, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Akhter, N., Antonellis, A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
Center project name: dhz
Center clone name: 355A20
                                                       Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: NIH Intramural Sequencing Center code: NISC
Consensus quality: 196656 bases at least Q40 Consensus quality: 197883 bases at least Q30
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by the finished sequence as soon as it is available and the accession number will be preserved.

1 28306: contig of 28306 bp in length 28307 28406: gap of unknown length 28407 37856: contig of 9450 bp in length 37857 37956: gap of unknown length 37857 37956: gap of unknown length 37957 73522: contig of 35566 bp in length 73523 73622: gap of unknown length 73523 383567: contig of 9945 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       consists of 12 contigs. Gaps between the are represented as runs of N. The order c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            provided by the submittor. This sequence will be replaced
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159879: contig of 34168 bp in length
159979: gap of unknown length
174698: contig of 14719 bp in length
174798: gap of unknown length
18482: contig of 11584 bp in length
186482: gap of unknown length
193344: contig of 6862 bp in length
193344: gap of unknown length
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|--|--|--|--|---|--|---|---|--|--|--|--|--|--|---|--|--|--|--|
| 961 GA | 901 GG | 841 GT 1 68950 GT | 781 Cc 69010 Tc | 721 AT 69070 AT | 661 TG | 601 GG 69190 GG | 541 TC 69250 TC | 481 TA - 69310 TA | 421 GA 69370 GA | 361 GA 69373 | 301 AA 69373 | 241 CA 69431 CA | 181 CG 69491 CG | 121 CT 69551 CT | 61 TA 69607 TA | 7 | tch als 1907 | |
| TGTGGAGA | CGGAGAGA CGGAGAGA | GTCCAGTA | TATTTTTG | CCAGCTTC CCAGCTTC | CCAAGTGT CCAAGGGT | AGACATTT | CAAGCGAA | TTATAGGA | GGAAGGAA AGAAGGAA | AAGAAAGG | AGGAAGGA | AAGCAAGA AAGCAAGA | TTTGAGGC | TGCACCTG | AAGAGATA AAGAGATA | ACAGACCA ACAGACCA | imilarity ; Conserva | 49975 a 4 |
| GGAAGGGT | TACACGATO | AGAGAAATI AGAGAAATI | CAGAAGGGI CAGAAGGGI | AGATGCCC/ AGATGCCC/ | GCTGTTCA GCTGTTCA | TTGGTTGTO TTGGTTGTO | TGGATTTC: TGGATTTC: | GGGTAATTI GGTAATTI | GGAAAGAA GGAAGGAA | AAGAAAGA(| AGGAAGGA | CGTTTTTG: ACTTTTTG: | TGCGGTAA(TGCGGTAA(| TAGTTCCA(TAGTTCCA(| TAAAGAGATAGATATATGTACTAAATTA | AAAACTTCO AAAACTTCO | 81.4%; 92.0%; tive | 9805 c 4 |
| CACAGACCC | BAGGGAGAC BAGGGAGAC | AAGGCCTGC AAGGCCTGC | AGGTATAAG AGGTATAAG | ACAGTGCCC ACAGTGCCC | ACATGCTAT | CACAACTAT | PATTGGGAG PATTGGGAG | ATAGGGAGG ATAGGGAGG | GAAAAGAG GAAAAGAG | BAAAGAAAG | BAAAGAAAG | CAGAAAGA CAGAAAG | SCCATGACT | CTACTTGG | CGTAGTAAA CGTAGTAAA | TIGCCGCGT | Score 1686.8; Pred. No. 0; 0; Mismatches | 18502 g |
| CCCCGAAA | AGGCTGGA | ACAGGCTG ACAGGCTG | GATGGGTT GATGGGTT | AGATCGAG AGATCGAG | GATGCACA | ATGGAGGG ATGGAGGG | TGATTCTG | TATGGGGA | GGAAAAA GGAAAAA | AAAAAGAA | GAAGGAAG | AAAAAAAA AAAAAAAA | GCACTGCT | GAGGCTGA | ∨ ب | GGACCTCA GGACCTCA | | 51409 t |
| TGATGTGTG | ACAGAAAGI ACAGAAAGI | GAGGGGAG! GAGGGGAG! | GGTGGAGA/ GGTGGAGA/ | GAACCCTC! AAGCCCTC! | CGGCAGGC CGGCAGGC | GCATTACTO GCATTACTO | CCCTAGA/ CCCTAGA/ | ATTGAAGAO ATTGAGGAO | ATGACTGTT | AGAAAGAA! | GAGAAAGA! | AGAGACGA! AGAGACGA! | SCACTCCAC | GGTGGGAG <i>I</i> GGTGGGAG <i>I</i> | AAAAAAAAATTAGCC AAAAAAAAATTAGCC | IGTTCCCC! | DB 2; Le 37; Inc | 1101 ot |
| ATGTGGAGAGGAAGGGTCACAGACCCCCCCGAAATGATGTGTGGGACAACAGGAATCTGG | GCGGAGAGATACACGATGAGGGAGACAGGCTGGAACAGAAAGTAGAGACGAAGATTCGA | GTGTCCAGTAAGAGAAATAAGGCCTGCACAGGCTGGAGGGGAGAGTGAGAGAGA | CGTATTTTTGCAGAAGGGAGGTATAAGGATGGGTTGGTGGAGAATGGGGAAGGAAGGTG | ATCCAGCTTCAGATGCCCACAGTGCCCAGATCGAGGAACCCTCATCCAGGGGCTGAGAAC | TGCCAAGTGTGCTGTTCAACATGCTATGATGCACACGGCAGGCCTCCACAACAACCATT | GGAGACATTTTTGGTTGTCACAACTATATGGAGGGGCATTACTGGCAACTAATGGATAGA | TCCAAGCGAATGGATTTCTATTGGGAGTGATTCTGCCCCTAGAAGACACTGGCAATACCA | TATTATAGGAGGTAATTATAGGGAGGTATGGGGAATTGAAGACAGAAACACAAATTAG | AGGAAGGAAGGAAAGAAGGAAAAGAGGGAAAAAATGACTGTTGAAGAGCAGTGAGTAT | AAAGAAAGGAAAGAAAAGAAAGAAAAGAAAGAAAGAAA | aaaggaaggaaggaaggagaaaggaaggaaggaaaggaaaggaaaggaaaggaaggaaggaaggaaggaaggaaggaaggaaggaaggaaggaaggaaggaaggaaggaa | BAAGCAAGACGTTTTGTCAGAAAGAAAAAAAAAAAGAGACGAAGGGAAGGAA | CGTTTGAGGCTGCGGTAAGCCATGACTGCACTGCTGCACTCCAGACAGCAGCCTGGGTGA | TTGCACCTGTAGTTCCAGCTACTTGGGAGGCTGAGGTGGGAGAATTGCTTGAGCCCAAA | AAAGAGATAGATAAATATCTAGTAAATTAAAAAAAAAAA | AAACAGACCAAAAACTTCCTGCCGCGTGGACCTCATGTTCCCCAAGTGGAAGACAGGCAA | Length 2007 Indels 128; | others |
| GAATCTGG | AGATTCGA AGATTCGA | GAAAGGGA GAAAGGGA | GAAGGTGT GAAGGTGT | CTGAGAAC CTGAGAAC | AAACCATT | TGGATAGA TGGATAGA | CAATACCA CAATACCA | CAAATTAG CAAATTAG | GTGAGTAT | AAAAGAGA agg | AGGAAGGA | GGAGAGAG | CTGGGTGA CTGGGTGA | AGCCCAAA AGCCCAAA | GGGTGTGGTGG AGGTGTGGTGG | ACAGGCAA ACAGGCAA | 792; ; Gaps | |
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| CCAAATTT CCAAATTT | ATCTCCCT | CTCTCTAG | CCCCTGAC | TGACACTO | ACTCCTGA AACTCCTGA | CEGETETO | ATGGCTCC | GCCTCTCT | TCCATCTA | TTTTCTGC | AGTGAAAT | | GCGCTCCA | | | | AGAGGAAG | ATGTGGAG |
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| | AAGCTCAG | TTTCCAAA | CAGGGTCC | CTTCCCAG | CACACCGG CACACCGG | GTTCACCAL GTTCACCAL | CTGGGGAG | CCTGCAGG | CTCATGTC: | CTTTCCATC | TCTCTCTCT | AGACTCCA: | HIIIIIIII | TGGACACC | TGGACACC | ATACTTTGO CAACATGGO | | CCCCCGAA |
| 2071 67723 | 360001 | ACTGTC | SCTTCC GCTTCC | GATGT | CATCCC | AGTGGAT | ATTACCC | TEATTC | ICCITCE | TOTOTOTO | TTTTGC | CTCA | CTCAAA | CTGCAG | TGAAACC | HIIIII BAGGCTG | CTGAAG | ATGATGT |
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/mol_type="genomic DNA"
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Eukaryota; Metazoa; Chordata;

Craniata; Vertebrata; Euteleostomi;

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Email: myers@shgc.stanford.edu
Primer A: AGAGACACGGTCAGCCCAAT
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Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford
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OS Homo sapiens (human)

PN J 2002507387-A/94

PD 12-MAR-2002

PF 22-DEC-1998 JP 2000526543

PR 24-DEC-1997 US 08/998253,24-DEC-1997 US 08/998255 PR

17-JUL-1998 US 09/118524 PI STEVE

G REED, JIANCCHUN XU

PC C12N15/09, A61K38/00, A61K39/00, A61K39/39, A61K39/395, A61P35/00, PC C07K14/47,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reed, S.G. and Xu, J.
Compounds for immunotherapy and diagnosis
methods for their use
Patent: JP 2002507387-A 94 12-MAR-2002;
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Compounds for immunotherapy and diagnosis
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                Submitted (19-APR-2003) Pathology and Laboratory Medicine, Mount Sinai Hospital, 600 University Avenue, Toronto, Ontario M5G 1X5,
                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 1370)
Kurlender, L., Yousef, G.M.,
and Diamandis, E.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kurlender,L., Yousef,G.M.,
and Diamandis,E.P.
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/codon_start=1
/product="Rallikrein 5 splice variant 1"
/protein_id="Aap42275.1"
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GSNQDLGAGAGEDARSDDSSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQW
                                                                                       similar to the AF135028"
                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="19"
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                                                                                                              /note="serine
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Borgono, C.A.

Borgono, C.A.

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KEYWORDS
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36 human secreted proteins.
BD107879
                                                       Ruben, S.M., Soppet, D.R., Ebner, R., Lafl Brewer, L.A., Olsen, H.S., Duan, R.D. and 36 human secreted proteins Patent: JP 2002500035-A 50 08-JAN-2002, HUMAN GENOME SCIENCES INC
                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1381)
Homo sapiens
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                           Homo sapiens (human) JP 2002500035-A/50
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/gene="KLK5"
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RRIRPTKDVRPINVSSHCPSAGTKCLVSGWGTTKSPQVHFPKVLQCLNISVLSQKRCE
DAYPRQIDDTMFCAGDKAGRDSCQGDSGGPVVCNGSLQGLVSWGDYPCARPNRPGVYT
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ACCESSION VERSION KEYWORDS

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SKODGAGAGEDARSDDSSSRIINGSDCDMHTQPMQAALLLRENQLYCGAVUVHPQW
LLTAAHCRKKVERVRLGHYSLSPVYESGQQMFQGVKSIPHPGYSHPGHSNDLMLIKL
RRIRPTKDVRPINVSSHCPSACTKCLVSGWGTTXSPQVHFPKVLQCLNISVLSQKRCE
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/protein_id="AAF03101.1"
/db_xref="GI:6063033"
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/note="SCTE; trypsin-like
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and Diamandis,E.P.
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Mammalia; Eutheria; Primates;
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/note="serine protease; differentially expressed in malignancy; may play a role in desquamation of skin; hK5; alternatively spliced; similar to the product of GenBank Accession Number AF135028"
                                                                            /product="kallikrein 5 splice variant 2"
/protein_id="App42276.1"
/protein_id="App42276.1"
/protein_id="App42276.1"
/db_xref="GI:31075483"
/translation="MATARPPMMWVLCALITALLLGVTEHVLANNDVSCDHPSNTVPS
/translation="MATARPPMMWVLCALITALLLGVTEHVQLYCGAVLLVHPQW
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/mol_type="mRNA"
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                   36 human secreted proteins
L Patent: JP 2002500035-A 51 08-JAN-2002;
HUMAN GENOME SCIENCES INC
OS Homo sapiens (human)
PN JP 2002500035-A/51
PN JP 2002500035-A/51
PD 08-JAN-2002
PF 06-JAN-1999 JP 2000527554
PF 07-JAN-1998 US 60/070657,07-JAN-1998 US 60/070658 PR 07-JAN-1998 US 60/070692,07-JAN-1998 US 60/070704 PI STEM RUBEN, DANIEL R SOPPET, REINHARD EBNER, DAVID W LAFLEUR, PI JIAN NI,
NI, LAURIE A BREWER, HENRIK S OLSEN, ROSANNE D DUAN, CRAIG A ROSEN PI LAURIE A BREWER, HENRIK S OLSEN, ROSANNE D DUAN, CRAIG A ROSEN PI LAURIE A BREWER, HENRIK S OLSEN, ROSANNE D DUAN, CRAIG A ROSEN PI LAURIE A BREWER, HENRIK S OLSEN, ROSANNE D DUAN, CRAIG A ROSEN PI LAURIE A BREWER, HENRIK S OLSEN, ROSANNE D DUAN, CRAIG A ROSEN PI LAURIE A BREWER, HENRIK S OLSEN, ROSANNE D DUAN, CRAIG A ROSEN PI LAURIE A BREWER, HENRIK S OLSEN, ROSANNE D DUAN, CRAIG A ROSEN PI LAURIE A BREWER, HENRIK S OLSEN, ROSANNE D DUAN, CRAIG A ROSEN PI LAURIE A BREWER, HENRIK S OLSEN, ROSANNE D DUAN, CRAIG A ROSEN PI LAURIE A BREWER, HENRIK S OLSEN, ROSANNE D DUAN, CRAIG A ROSEN PI LAURIE A BREWER, HENRIK S OLSEN, ROSANNE D DUAN, CRAIG A ROSEN PI LAURIE A BREWER, HENRIK S OLSEN, ROSANNE D DUAN, CRAIG A ROSEN PI LAURIE A BREWER, HENRIK S OLSEN, ROSANNE D DUAN, CRAIG A ROSEN PI LAURIE A BREWER, HENRIK S OLSEN, ROSANNE D DUAN, CRAIG A ROSEN PI LAURIE A BREWER, HENRIK S OLSEN PI LAURIE A BREWER PI LAURI
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Ruben, S.M., Soppet, D.R., Ebner, R., Lafleur, D.W., Ni, J., Brewer, L.A., Olsen, H.S., Duan, R.D. and Rosen, C.A.
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US-08-757-223-7
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US-09-818-512-3
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                                                                                                                                                                                                                                                                                                                                               569978 seqs, 220691566 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                            nucleic search, using sw model
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Maximum DB seq length: 200000000
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Sequence 18,
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Sequence 43,
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Patent No. 587237

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Kronmal, Gregory S.

APPLICANT: Lauer, Peter M.

APPLICANT: Thomas, Winston

APPLICANT: Thomas, Winston

APPLICANT: Tsucdihashi, Zenta

APPLICANT: Wolff, Roger K.

TITLE OF INVENTION: Megabase Transcript Map: No. 587223

TITLE OF INVENTION: Sequences and Antibodies Thereto

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOWNSEND and TOWNSEND and CREW LLP
                US-07-906-871-15
US-08-451-778A-7
US-08-451-778A-7
US-08-451-778A-7
US-08-998-208-7
PCT-US95-06743-7
US-09-913-817-3
US-09-913-817-3
US-09-918-512-3
US-09-918-512-3
US-09-818-512-3
US-09-813-3
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US-09-875-223-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
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not relevant
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TELEPAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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59065
12394
116592
162450
40000
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STRANDEDNESS: not
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                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
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80.1%; Pred. No. 3.1e-81;
ive 0; Mismatches 120;
                   LLP
                 TOWNSEND and CREW
                                    Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                   UMBER: US/08/724,394A
                                                                                                                                                                                                                                                                           CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: FILLS, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/POCKET NUMBER: 0179;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                               COUNTAL.
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
ACHUM TYPE: Floppy disk
ACHUM TYPE: Floppy disk
ACHUM TYPE: ACHUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
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                   TOWNSEND and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 80.1
Matches 580; Conservative
CORRESPONDENCE ADDRESS
                                                      San Francisco
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                                                                                                                                                                                                                                                              FILING DATE:
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                                                                                                                            3130 GCCCGGCTAA-TTTTTTTTTTTTTTAGTAGACGGGGTTTCACCGTTTTAGCCGGGATG 3072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2734 GGAGAATCGTTTGAACCTGGGACGTGGGGATTGCAGTGAGCCAAGACTGCACCACTGCAC 2675
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                                                        Gaps
                 Length 246240;
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Sequences and Antibodies Thereto
31
                                                    0; Mismatches 120;
                   Score 444; DB 2;
                                3.1e-81;
                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/08724394A
Patent No. 587237
APPLICANT: Feder, John N.
APPLICANT: Frommal, Gregory S.
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Thomas, Winston APPLICANT: Tsuchihashi, Zenta APPLICANT: Tsuchihashi, Zenta APPLICANT: Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ruddy, Deter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transitumes of INVENTION: Server
               22.2%;
80.1%;
                                                    580; Conservative
                                  Similarity
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US-08-724-394A-21/c
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                                                                                         395 TCGCCCAGGCTGGAGTGCAGTGGCGGGATCTCGGCTCACTGCAAGCTCCGCCTCCCGGGT
 24; Gaps
                                            No. 5872237el
Mismatches 120; Indels
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Sequences and Antibodies Thereto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lauer, Peter M.
Ruddy, David A.
Thomas, Winston
Tsuchihashi, Zenta
Wolff, Roger K.
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 Matches 580; Conservative
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ADDRESSEE: TOWNSEND a
STREET: Two Embarcade
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APPLICANT: Feder,
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US-08-724-394A-20
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APPLICANT:
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APPLICANT:
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                                                            935 CGAGAGTCACTTGAACCCTGGAGGCGGAGGTTGCAGTGGGCCCGAGATCACCATCACCGCCC 994
                                                                                                                         AAAATCAGCCGGGTGTCGTGGGGCCACCTGTAATCCCAGCTATGCTGGAGGCTGAGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Wegabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/724,394A FILING DATE: 01-OCT-1996 CLASSIFICATION: 536
Score 444; DB 2;
Pred. No. 3.1e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSEE: TOWNSEND and TOWNSEND and CREW : Two Embarcadero Center, 8th Floor San Francisco
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ATORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELEPHONE: 415-576-0200
TELEPHONE: 415-576-0300
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LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                                                   Sequence 22, Application US/08724394A Patent No. 5872237 GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kronnal, Gregory S. APPLICANT: Lauer, Peter M. APPLICANT: Ruddy, David A. APPLICANT: Thomas, Winston APPLICANT: Tsuchihashi, Zenta APPLICANT: Wolff, Roger K. TITLE OF INVENTION: Sequences arrITLE OF INVENTION: Sequences are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: not relevant
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80.1%;
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ADDRESSEE: TOWNSEND
STREET: Two Embarcad
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3123 AGCCGGGCGTAGTGGCGGGCGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCAGAGAA 3182
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881 AGCCGGGTGTCGTGGGGCACACCTGTAATCCCAGCTATGCTGGAGGCTGAGGCACGAGGAG 940
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Pred. No. 2.7e-68;
0; Mismatches 141;
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; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Tsuchihashi, Zenta
Wolff, Roger K.
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Best Local Similarity 76.6%;
Matches 553; Conservative
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Ruddy, David A.
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
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Pred. No. 2.7e-68;
0; Mismatches 141;
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| LOGATION: 1..246240

| GTHER INFORMATION: /note- "HLA-H.CONTIG"

US-08-724-394A-20
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                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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not relevant
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76.6%;
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Best Local Similarity 76.6
Matches 553; Conservative
                                                                      ZIP: 94111-3834
COMPUTER READABLE FORM:
San Francisco
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MOLECULE TYPE:
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701 CCATCAGACTCTACCCTTTAAATATGCAGTTTGGGCCAGGCACGCTGGCTCATGCCTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 246240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                       MEDIUM TYPE: FIOPPy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: UJ-0CT-1996
ATTONEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REGISTRATION NUMBER: 35,136
REGISTRATION NUMBER: 35,136
RELEFRORMICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAM: 415-576-0200
INFORMATION FOR SED ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 24640 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.0%; Score 380.4; DB 2; ilarity 76.6%; Pred. No. 2.7e-68; Conservative 0; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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Best Local Simil
Matches 553; C
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2965 TTTTTAT------CTAAAAAGTCTTTATAAAGGCCGGGCGGGGGCGTCGCCTCACGCTGTA
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APPLICANT: Feder, John N.
APPLICANT: Eduer, Peter M.
APPLICANT: Lauer, Peter M.
APPLICANT: Touch, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 587223
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: TOWNSEND and TOWNSEND and CREW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/08724394A Patent No. 5872237 GENERAL INFORMATION:
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COUNTRY:
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| Db 49932 GGTCAGGAGTTCAAGACCAGCCTGACCAACATGGAGAAACCCGTCTTACT 49881 Qy 862 AAAAAAAAAAAAAAATCAGCGGGTGTCGTGGGGGACCTGTAATCCTGTTGT 921 Db 49880AAAATACAAATTAGCCAGGTGGGGGAGGTGAATCCCAGCTACTG 49826 Qy 922 GGAGGCTGAGGCACGAGAGTCACTGAACCTGGAGGGGGGGG | Qy 1041 AACA 1044 1 | DENGTH: 84495 | Query Match Best Local Similarity 69.9%; Pred. No. 5.5e-65; Matches 545; Conservative 0; Mismatches 209; Indels 26; Gaps 3; Qy 357 TTTTTTTTTTTTTTTTGGGACTCCCCTCTCCCCCAGCTGGAGTCCAGT 416 | 417 GCGGGATCTCGGCTCACTGCAGCTCCGCGTCTCGCGGTTCACGCCATCTCCTCGCCTCAG 1 | OY 477 CCTCCCAAGTAGCTGGGACTACAGGCGCCCGCCACTACGCCCGGCTAATTTTTGTATT 536 | 38207 597 38147 | 657 CATGATCTTCTTGACTATGCTGATGAGAAGTACCTAAAGCCAT | QY 705 CAGACICTACCTITAAATATGCAGCCAGGCACCGTGGCTCAFGCCTGTAATTC 764 |
|---|--|--|---|---|--|---|--|--|
| Qy 941 TCACTTGAACCCTGGAGGCGCAGGTTGCAGTGGGCCGAGATCACACCACCTCCAGC 1000 Db 3183 TGGCGTGAACCCGGGAGGCTTGCAGTGAGCCGAGATCCCGCACTGCACTCCAGC 3242 Qy 1001 CTGGGCGACAGAGCACTGTCTCAAATAAATAAACAAACGAACACAGACAG | RESULT 7 US-09-81-896-3/C US-09-81-896-3/C Sequence 3, Application US/09851896, Patent No. 6410325 Patent No. 6410325 APPLICANT: C. Frank Bennett APPLICANT: Susan M. Freler APPLICANT: Andrew T. Watt TITLE OF INVENTION: EXPRESSION TITLE OF INVENTION: EXPRESSION TITLE OF INVENTION: EXPRESSION TITLE OF INVENTION: EXPRESSION TITLE OF INVENTION: BAPPLICATION NUMBER: US/09/851,896 CURRENT APPLICATION NUMBER: US/09/851,896 CURRENT FILING DATE: 2001-05-08 SEQ ID NO 3 LENGTH: 70000 TYPE: DNA OFFENDIA FRAURE: US-09-851-896-3 | Query Match 18.3%; Score 366.4; DB 4; Length 70000; Best Local Similarity 74.0%; Pred. No. 1.4e-65; Matches 536; Conservative 0; Mismatches 146; Indels 42; Gaps 4; QY 349 TITITITITITITITITITITITITITITITIAGACGGAGTCTCGCTCTGCCCCAGGCTGA 408 | QY 409 GTGCAGGGGGGGATCTCGGCTCACTGCAAGGTCCGGCTTCACGCCATTCTCC 468 111111111111111111111111111111111111 | 529 TITGIALITITAGRAGACGCGGTTCACCGTTTTAGCCGGGATGCCTCGATCTCTG 111111111111111111111111111111111 | Oy 589 ACCTGGTGATCCGCCCCGCCTCCCCAAGTGCTGGGATTACAGCGTGAGCCACG 648 Db 111111111111111111111111111111111111 | DD 50112 CGCCCTGCATTGGTTACGTTGGCACTGGATGGATGGATGG | 742 ACCGIGGCICATGCCIGIAAITCCAGCACITIGGGAGGCAGAGGIGGGTGAATCACTIGA | OY BOZ GGCCAGGAGTTTGAGACCAGGCCAACATGGTGAAACTCTGTTTACTAAAAAA B61 |

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07-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-367-841A-43/C
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                                       37908
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                                                                             37907 GGGCAACATAGGAAGACTCTGTCTCT-----AAAAAAAATTAAAATTAGCC
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                    CAGCACTTTGGGAGGCAGAGGTGGGTGAATCACTTGAGGCCAGGAGTTTGAGACCAGGCT
                                                          885 GGGTGTCGTGGGGCCACACCTGTAATCCCAGCTATGCTGGAGGCTGAGGCACGAGAGTCAC
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COTHER INFORMATION: EXON: 14539-14581; INTRON: 6791-11583; INTRON: 5. OTHER INFORMATION: 11676-14538; CDS: 11584-11675; 14539-14580
05-08-520-373D-4
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0; Mismatches 97; Indels
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                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08520373D Patent No. 6451763
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Best Local Similarity 76.3%;
Matches 528; Conservative
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ORGANISM: HUMAN
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                    765
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                     659 TGATCATCTTCTTGACTATGCTGATGTGACAAGTACCTAAAGCCATCAGACTCTACCTT
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TCCCAAGTAGCTGGGACTACAGGCGCCCGCCACTACGCCCGGCTAATTTTTTGTATTTT
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TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
STREET: 345 Park Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1019 CTCTGTCTCAAATAAATAAATAAACAAACGAA 1050
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Patent No. 6319687
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Rodriguez,
APPLICANT: Tombran-Tink, Joyce
APPLICANT: Tombran-Tink, Joyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/367,841A
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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1019 CTCTGTCTCAAATAAATAAATAAACAAACGAA 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 22481 Base Pairs
Nucleic Acid
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                                                                                                                                                                                                                                                                                                                             345 Park Avenue
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                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unknown
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                                                                                                                                                                                                                                                                                                                                                                     New York
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                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                           RESULT 11
PCT-US95-07201-43/c
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 10154
                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                    NAME: DOROTHY R. AUTH
RECISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126US2
TELECOMMUNICATION INFORMATION:
             APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                       TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 22481 Base Pairs
TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                           MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 18.19
Best Local Similarity 76.37
Matches 528; Conservative
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                          Unknown
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                                                                                                                                                                                                                                                           TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 22481;
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18.1%; Score 362.8; DB 5
76.3%; Pred. No. 5.9e-65;
ive 0; Mismatches 97
                                                                                                                                                                                            Sofia
                                                                                                                                                                                    APPLICANT: Chader, Gerald J.; Becerra, S
APPLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Taniwaki, Takayuki
                                                                                                                                                                                                                                                                                                                                                                                        Morgan & Finnegan, L.L.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US95/07201
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07/UN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                    Sequence 43, Application PC/TUS9507201 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
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APPLICATION NUMBER: 08/367,841
FILING DATE: 30-DEC-1994
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Best Local Similarity
Matches 528; Conserv
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             Query Match
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APPLICANT: No. 6391850thwestern University
APPLICANT: No. 6391850thwestern University
APPLICANT: No. 63918501 Bouck
APPLICANT: Paul Gillis
APPLICANT: Paul Gillis
TITLE OF INVENTION: Methods and Compositions for
FILE REFERENCE: 0290-23U3
CURRENT APPLICATION NUMBER: US/09/875,223
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 09/122,079
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1997-07-23
SOFTWARE: PALOR NUMBER: US 08/899,304
PRIOR FILING DATE: 1997-07-23
INUMBER OF SEQ ID NOS: 2
SOFTWARE: PALENTIN VET: 2.1
SEQ ID NO 2
ILENGTH: 22484
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Patent No. 6391850
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LOCATION: 1...22484
COTHER INFORMATION: "n" means
US-09-875-223-2
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US-09-875-223-2/c
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                                     Gaps
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APPLICANT: Poduslo, Shirley E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ASSESSING RISK TITLE OF INVENTION: FACTORS IN ALZHEIMER'S DISEASE NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
Length 22484;
                                     Indels
     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 362.8; DB 4
Pred. No. 5.9e-65;
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                                   0; Mismatches
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2200 Ross Avenue, Suite 2200
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STREET: 2200 ACC.
STREE: Texas
STRTE: Texas
ZIP: 75201-6776
COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"MUTTER: IBM PC COMPATIBLE
"""FM; PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-757-223-7; Sequence 7, Application US/08757223; Patent No. 6136530
   18.1%;
76.3%;
                                     Conservative
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31866
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                                                                                                                       APPLICANT: BEASLEY, Ellen M. et al
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001213
CURRENT APPLICATION NUMBER: US/09/820,924
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTERO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         964 GIIGCAGIGGGCCGAGAICACAICACCGCCCTCCAGCCTGGGCGACAGAGCAAGACTCTG 1023
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Pred. No. 5e-63;
0; Mismatches 149; Indels
                                                                          Sequence 3, Application US/09820924
Patent No. 6555351
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 72.8%;
Matches 549; Conservative
 1792 GTGTGGTGGTGC 1803
                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Human
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LENGTH: 39982
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Pred. No. 3.2e-63;
0; Mismatches 134;
SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,223
                                APPLICATION NUMBER: US/08/757,223 FILING DATE: No. 6136530ember 27,
                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MAYfield, Denise L.
REFERENCE/DOCKET NUMBER: 4-00
TELEPHONE: 214/740-8785
TELEPHONE: 214/740-8785
TELEFAX: 214/740-8800
                                                                                                                                                                                                                                                                                               Query Match 17.7%;
Best Local Similarity 75.3%;
Matches 551; Conservative
                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 5375 base pairs
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US-08-757-223-7
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Search completed: August
Job time: 139.698 secs
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                                                                                                                                             GENERAL INCORNATION:
APPLICANT: BEASLEY. Ellen et al.
APPLICANT: BEASLEY. Ellen et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFRENCE: CLOOI192
CURRENT APPLICATION NUMBER: US/09/818,512
CURRENT FILING DATE: 2001-03-28
NUMBER OF SQC ID NOS: 4
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 3
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Pred. No. 7e-61;
0; Mismatches 219;
                                                    31986 ТСТААААААТААТААТААТАААААААААТАААА 32019
                         1024 TCTCAAATAAATAAATAAACAAACGAACAAGCAG 1057
                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (1)...(116592)
; OTHER INFORMATION: n = A,T,C or G
US-09-818-512-3
                                                                                                                      Sequence 3, Application US/09818512
Patent No. 6537780
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 17.2%;
Best Local Similarity 65.8%;
Matches 615; Conservative
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ORGANISM: Human
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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| OM nucleic - nucleic search, using sw model | August 4, 2003, 21:01:54; Search time 7120.12 Seconds (without alignments) 11491.278 Million cell updates/sec | US-09-936-271B-13_COPY_1_2000 2000 1 999cccagagtgaaggcaaggtgcgtcctgcacccacatc 2000 | IDENTITY_NUC Gapop 10.0 , Gapext 1.0 |
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| OM nucleic - nu | Run on: | Title: Perfect score: Sequence: | Scoring table: |

Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

2888711 seqs, 20454813386 residues

Searched:

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| | ens kallikrein-like | AF135028.1 GI:4589282 | Homo sapiens (human) Homo sapiens | Eukaryota; Metazoa; Chordata; |
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 11570)
Yousef,G.M. and Diamandis,E.P.
The new Kallikrein-like gene, KLK-L2. Molecular characterization, mapping, tissue expression, and hormonal regulation

REFERENCE AUTHORS TITLE

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                                                                                         Yousef,G.M., Luoi.Y. and Diamandis,E.P.
Direct Submission
Submitted (13.MAR-1999) Pathology and Laboratory Medicine, Mount
Sinai Hospital, 600 University Avenue, Toronto, Ontario M5G 1X5,
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                           2 (bases 1 to 11570)
Diamandis,E.P., Yousef,G.M., Luo,L.Y., Magklara,A.
The new human kallikrein gene family: implications
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| enomic DNA" con:9606" 119" 147C22" | Andre-NOTE: Sharter libraries falled to resolve dinucleotide repeat. Unsure number of repeat copies 64998-65494. Forced join 65015." BASE COUNT 26044 a 27304 c 25728 g 28411 t | Query Match 99.5%; Score 1989; DB 9; Length 107487; Best Local Similarity 100.0%; Pred. No. 0; Matches 2000; Conservative 0; Mismatches 0; Indels 1; Gaps 1; | Oy 1 GGGCCCAGAGTGAAGGCAAGAGGGTTGAGACTCCCTCTGCAAAGTGGCTTGAGTC 60 | Qy 61 TCCCTGCCTAAAATGCAGGGAGGGAGGCAGAAGACAGGGA-GAGGAAGGGGTGGG 119 | OY 120 GAAGAAAGAGAGAGAGAGAGAGACAGAATAACACAACTACAGAAACACAGAGAACA 179 | OY 180 CACAGAGACCTGGGACACAGGGACACACAGAGTCAGAGAAAAGAGAAAGAGAAAA 239 | Qy 240 GACACAAATGGAGACACAGAGTGTAAAGAAAAGAGAGATTAACAGAGTCCCAGATACACG 299 | QY 300 CAAAGGGCAGAAGCACAGTTTTCAGGGTGGTGTCTATGATCATCTTTTTTTT | Db 59860 TITITITITITITITICAGACGGAGTCTCGCTCTGTCGCCCAGGCTGCAGTGCAG | 480 CCCAAGTAGCTGGGACTACAGGCGCCCGCCACTACGCCCGGCTAATTTTTTTT | OY 540 AGTAGAGACGGGGTTTCACCGTTTTAGCCGGGATGCCTCGATCTCCTGACCTCGTGATC 599 | , by 600 cgcccgccTcGgccTcCcAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCAT 659 | OY 660 GATCATCTTGACTATGCTGAGAGAGTACCTAAAGCCATCAGACTCTACCTTT 719 | QY 720 AAATATGGAGTTTGGGCCAGGCACCGTGGCTCATGCCTGTAATTCCAGCACTTTGGGAGG 779 | OY 780 CAGAGGTGGGTGAATCACTTGAGGCCAGGAGTTTGAGACCAGCTGGCCAACATGGTGAA 839 | Qy 840 ACTCTGTCTTTACTAAAAAAAAAAAAAAAAAAAAAAAAA |
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| | 1521 | QY 1681 GTAGGGAGTGACATTCCGGACTGGGGGGGGTGCTCTGGGGGGGG | Qy 1741 GGAGGAGCTATTGCTAAGGCCCGATAGGCACCTCATTGCCCGGGAATGTGCCCCAGGGAG 1800 1741 GGAGGAGCTATTGCTAAGGCCCGATAGGCACCTCATTGCCCGGGAATGTGCCCAGGGAG 1800 | Qy 1801 CAGTGGGTGGTTATATACTCAGGCCCGGTGCCCAGAGCCGGGGGGGG | QY 1861 AGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAATCCCCCACCCCTACCTGG 1920 Db 1861 AGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCCACCCCTACCTGG 1920 | Qy 1921 GGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGGAAGGAGAGGTGTCT 1980 Db 1921 GGGACAGGGCAAGTGAGCTGGTGAGGTGGCTCAGCAGGCAG | OY 1981 GTGCGTCCTCCACATC 2000 . | 2 3/c AC011483 ION Homo sapiens ON AC011483 | VERSION AC011483.7 GI:21637461 KEYWORDS HTG. SOURCE HOMO sapiens (human) ORGANISM HOMO sapiens Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: | Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 107487) AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center. TITLE Direct Submission | Upper Supply of the control of the c | REFERENCE 3 (bases 1 to 107487) Mitchell Drive, Walnut Creek, CA 94598, USA AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center. | ΑΓ | www.jgi.doe.gov Finishing Completed at Stanford Human Genome Center www.sigc.scmpleted at Stanford Human Genome Center www.sigc.stanford.org.scm.scm.scm.scm.scm.scm.scm.scm.scm.scm | Estimated Total Number of Errors 18 0.6. NOTE: Shatter libraries failed to resolve dinucleotide repeat. Unsure number of repeat copies 64998-65494. Forced join 65015. | FEATURES LOCALION/QUALILIERS SOUICE 1107487 /organism="Homo sapiens" |

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                                                                                                      AF243527 230000 bp DNA linear PRI 21-NOV-2000 Homo sapiens serine protease gene cluster, complete sequence. AF243527
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COMPLEMENT (John (13552. 13704, 14377. 14530, 14678. 14917, 15416. 15569, 19204. >19246))
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I (bases 1 to 230000)
Gan.L., Lee.I., Smith, R., Argonza-Barrett, R., Lei, H., McCualg, J., Moss, P., Paeper, B. and Wang, K.
Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region
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Gan.L., Lee.I., Smith.R., Argonza-Barrett,R., Lei,H., McCuaig,J. Moss.P., Paeper.B. and Wang,K.
Direct Submission
Submitted (09-WAR-2000) Chiroscience R & D Inc., 1631 220th St.
Bothell, WA 98021, USA
Location/Qualifiers
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                                                                                                                                            TCTGTCTCAAATAAATAAATAAACAAACGAACAAGCAGTTTGTTGTACTTAGTTATATC
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142548 GGGCCCAGAGTGAAGGCAAGAGAAGAGTTGAAGGCTCCCTCTGCAAAGTGGCTTGAGTC 142489
                                                                                                                                                /protein_id="AAG33359.1"
/db_xref="GI:11244764"
/translation="MKKLMVVLSLIAAAWAEEQNKLVHGGPCDKTSHPYQAALYTSGH
                                                                                                                                                                                                                                      LLCGGVLIHPLMVLTAAHCKKPNLQVFLGKHNLRQRESSOEOSSVVRAVIHPDYDAAS
HDODINLLRARPAKLSELIOPLPLERDCSANTTSCHILGWGKTADGDFPDTLOCAYI
HLVBREECEHAY PGOLTGNMLCAGDEKYGKDSCQGDSGGPLVCGDHLRGLVSWGNIPC
GSKEKPGVTNVCRYINWIQKTIQAK"
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SDLMCVDVKLISPQDCTKVYRDLLENSMLCAGIPDSKKNACNGDSGGPLVCRGTLQGL
SSDLMCYDVKLISPQCKFTKWINDTMKKHR"
complement(join(<183943. 184098,185635. 185768,
187865. 188127,188293. 188452,188967. >189036))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"neuropsin"

protein_id="AAG33361.1"

db_xreff="G1:124766"
/translation="MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHEQQPHSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PWQAALFQGQQLLCGGVLVGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVO
SPIPPCYNDSDVDEDHNHDLMLLQLRDDASLGSKVRFISLADHCTQPGQKCTVSGWGTV
TSPRENFPDTLNCAPWIFPCKKCEDAYFQQITDGWVCAGSSKGADTCQGDSGGPLVC
DGALQGITSWGSDPCGKSDK RGVYTNLCRYLDWIKKIIGSKG"
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TLQCANISILENKLCHWAYPGHISDSMLCAGLWEGGRGSCQGDSGGPLVCNGTLAGVV
SGGAEPCSRPRRPAVYTSVCHYLDWIQEIMEN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="marsLLLPLQILLLSLALETAGEEAQGDKIIDGAPCARGSHPWQ
VALLSGNQLHCGGVLVNERWVLTAAHCKMNEYTVHLGSDTLGDRRAQRIKASKSFRHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MKLGLLCALLSLLAGHGWADTRAIGAEECRPNSQPWQAGLFHLT
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.146986,149628. .149764,
.155208,155948. .155987))
also called neurosin or zyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(165420. 165575,167672. 167808, 168124. 168124. 116871,169651. 169798,170211. .>170283))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(<190980. 191129,191573. 191709, 194324. 194589,197048. 197204,197370. >197412)) /product="kallikrein-like 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="stratum corneum chymotryptic enzyme" /product="stratum corneum chymotryptic enzyme" complement(join(166420. 165575,167672. 167808, 168124. 168311,169651. 169798,170211. 170283))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(183943. 184098,185635. 185768,
187865. 188127,188293. 188452,188967. 189036))
/note="serine protease; also called ovasin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(190980. 191129,191573. 191709, 194324. 194889,197048. 197204,197370. 197412))
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/protein_id="AAG33360.1"
/db_xreff="GI:11244765"
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/protein_id="AAG33362.1"
/db_xref="GI:11244767"
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100.0%; Pred. No. 0;
                                                             /note="serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="serine protease"
                                                                                                                       /product="protease M"
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                                                                                                                                                                                                                                                                                                                                                                                         /gene="KLK7"
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Matches 2000; Conservative
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                              .46235,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .64678
                                                                                     /product="prostate specific antigen"
join(42595. .42640,43880. .44039,45669. .45955,46099. .46235,
/gene="KLK3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="glandular kallikrein"
join(61139. .61184,62391. .62550,64142. .64428,64542. .64678,
56074. .66229)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNGVLGGITSRGPEPCALPEKRAVTRYVHYRKWIKDTIAANP"

COMPLEMENT(join(<94602. 94754,96027. 96163,96247. 96497,

96919. 97081,98345. .>98405))

/product="serine protease"

complement(join(94602. 94754,96027. 96163,96247. 96497,

96919. 97081,98345. 98405))
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VSWGDYPCARPNRFGVYTNLCKFTKWIOETTQANS"
comptement (join(<146834. 146986,149628. 149764,
151186. 151433,155052. 155208,155948. >155987))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MMDLVLSIALSVCCTGAVPLIOSRIVGGWECEKHSOPMOVAVYS
HGWAHCGGVLVHPQWVLTAAHCLKKNSQVWLGRHNLFEPEDTGORVPVSHSFPHPLYN
MSLLKHQSLRPDEDSSHDLMLLRLSEPAKITDVVKVLGLPTQEPALGTTCYASGWGSI
EPEEFLRPRSLQCVSLHLLSNDMCARAYSEKVTEFMLCAGLWTGGKDTCGGDSGGPLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation-*MatagnwgwFlGyLilGyagSlvSgScSgIlNGEDCSPHSQPW
AALVWBUELCSGYLVHPQWVLSAAHGFQNSYTIGLGLHSLEADDPGSGSWYEASLS
VRHBEYNRPLLANDLAH.
WHENEYNRPLLANDLAH.
MPTVLQCVNVSVVSEVCSKLYDPL#HSMFCAGGGHDQXDSCNGDSGGPLICKGYL
                                                                                                                                                                                                                                                                                                                                                                                      /translation="mwvpvvFLTLSvTw1gAapLILSR1vGGwECEKHSQPwQvLvAs
RGRavCGGvLVHPQwvLTaAHCIRNKSv1LLGRHSLFHPEDTGQvFqvFqH9LYD
                                                                                                                                                                                                                                                                                                                                                                                                                                             MSLLKNRFLRPGDDSSHDLMLLRLSEPAELTDAVKVMDLPTQEPALGTTCYASGWGST
EREPETLPTKLQCVDLHVISNDVCAQVHPQKVTKFMLCAGRWTGGKSTCSGDSGGPLV
CNGVLQGTTSWGSEPCALPERPSLYTKVVHYRKWIKDTIVANP"
<61.139, . >66.229
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PGYSHPGHSNDLMLIKLNRRIRPTKDVRPINVSSHCPSAGTKCLVSGWGTTKSPQVHF
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complement(join(131301. .131456,136310. .136443,
136529. .136785,137525. .137690,140255. .140303))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="stratum corneum trypsin-like serine protease"
/protein_id="AAG33358.1"
                           .42640,43880. .44039,45669. .45955,46099.
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66074. .>66229)
/gene="KIK2"
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136529. .136785,137525. .137690,140255. .>140303))
/gene="KLK5"
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complement(<131301. .>140303)
                                                                                                                                                                                                                                                                                                   specific antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="glandular kallikrein"
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/protein_id="AAG33355.1"
/db_xref="G1:11244760"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAG33356.1"
/db_xref="GI:11244761"
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/db_xref="G1:11244762"
                                                                                                                                                                                                                                         /note="serine protease"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="KLK2"
join'-7
                                                          47614. .>47769)
/gene="KLK3"
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| 12.18 PCCCCTGCTTAMANTGCAGGARANGGARANGCANAGGARAGGAGGARGANGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGACGAANAGGAANAGGAANAAANAAN | | Qy 1440 AGAACCAGAGAGAGGAGGAGAACTCTGAGAAAAAACCAGAGAGAG | 0y 1680 GGTAGGGACTGCACTTCCGCTGGGGGGTGCTCTGGGGGTGATAGGGGGAGC 1739 140868 GGTAGGGACTGACATTCCGGACTGGGGGGTGCTCTGGGGGACTAGGGGGAC 140808 GGTAGGACTTATCCTAGGCCCGATAGCCCCTTGGGGGTGGACTGGGGGACTAGGGGGAC 140809 0y 1740 AGGAGGACTATTGCTAGGCCCGATAGGCCCTATTGCCCGGGAATGTCCCCCAGGGA 14019 0y 1800 GGAGTGGTTATAACTCAGGCCCGATAGGCCCCAGAGCCCAGGAATGTCCCCCAGGGA 1859 111111111111111111111111111111111111 | RESULT 4 A027602 AC027602 AC027602 DEFINITION Homo sapiens chromosome 19 clone RP11-795B6 map 19, WORKING DRAFT SEQUENCE, 12 unordered pieces. ACCESSION ACCESSION AC027602 GI:11178143 KEYWORDS KEYWORDS HTG; HTGS.PHASEI; HTGS_DRAFT. SOURCE Homo sapiens CRGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. AUTHORS Birren, B. Linton, L., Nusbaum, C. and Lander, E. TITLE HOMO sapiens chromosome 19, clone RP11-795B6 |
|---|---|---|--|---|
| | TCCCCTGCCTAAAATGCAGGAGAGGAGGAGAAAAGGGAAGGAA | 360 TTTTTTTTTTTTTGAGACGGAGTCTCGCCCAGGCTGGAGTCCAGTGGCG 419 11111111111111111111111111111111111 | 600 CACCTGGTTAGCTTTGTGGGATTACGGGGTGAGCCACGGGCGAT 659 61948 CGCCGGCTCGGCCTCCCAAAGTGCTGGGATTACGGGCGTGAGCCACGGCCGGC | GGAGGTTGCAGTGGCCGAGATCACCACCGCCCTCCAGCCGGCGACAGAGCAAGAC 1019 GIGAGGTTGCAGTGGCCGAGATCACACACCACCCCTCCAGCCTGGGCGAILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII |

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Quality coverage: 10.7 in Q20.

NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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/clone_lib="RPCI-11 Human Male BAC"
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35535, .124474
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162444. .208917
/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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/db_xref="taxon:9606"
/chromosome="19"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

3. (bases 1 to 27346)

Birren,B., Linton,L., Nusbeum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar K., Diaz,J.S., Dodge,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pleirer,N., Hagos,B., Heaford,A., Horkon,L., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McKernan,R., MorPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Olivar,T.M., Oliver,J., Peterson,R., Piere,N., Pisani,C., Pollara,V., Raymon,C., Rieback,M., Riley,R., Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Trirell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Dirner, Shring, A., A and Cody,M.
                                                   S Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Cooke, P., Derarellano, K., Dowar, K., Diaz, J. S., Collymore, A., Cooke, P., Derarellano, K., Dowar, K., Diaz, J. S., Collymore, A., Cooke, P., Derarellano, K., Dewar, K., Diaz, J. S., Collymore, A., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand, Pierre, N., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karatas, A., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lancque, K., Landzares, R., Landers, T., Leu, C., Liu, G., Locke, R., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meddrim, J., Menneus, L., Minova, T., Miranda, C., Monnell, P., O'Neil, D., Olivar, T. M., Oliver, J., Peterson, K., Plerre, N., Peterson, K., Palamas, J., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Vassiliey, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M., Wyman, D., Ye, W. J., Chand, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Nov 15, 2000 this sequence version replaced gi:11136831. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Whitehead Institute/ MIT Center for Genome Research
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Sequencing vector: Plasmid; n/a; 69% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 213058 bases at least 030
Consensus quality: 213655 bases at least 030
Consensus quality: 215058 bases at least 020
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------- Project Information
Center project near: 19166
Center clone name: 795_B_6
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Insert size: 216246; sum-of-contigs
Quality coverage: 11.9 in Q20 bases; agarose-fp
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                                          (bases 1 to 217346)
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Length 217346;

| Db 202770 GGCCCAGGGAGTAGGAGTTCCGGACTGGGTGGGGGTTCTGGGGGTGGAGA 202711 Db 1730 TAGGGGAGCAGGAGTATTGCTAAGGCCCGATAGGCACTTGCCGGGAATGT 1789 1710 TAGGGGAGCAGCTATTGCTAAGGCCCGATAGGCACTTGCCGGGAATGT 1789 1790 GCCCAGGGAGCGTATTGCTAAGGCCCGATAGGCCCGGGAATGT 202651 Db 20250 GCCCAGGGAGCAGTGGTTATAACTCAGGCCCGTGCCCAGGAGGAGGC 1849 11111111111111111111111111111111111 | RESULT 5 AC130782 AC130782 AC130782 AC130782 DEFINITION Pan troglodytes clone CH251-355A20, WORKING DRAFT SEQUENCE, 12 DEFINITION PAC130782 AC130782.2 GI:25167101 VERSION VERSION AC130782.2 GI:25167101 KEYWORNS HTG: HTGS_PHASE2: HTGS_DRAFT. SOUNCE Pan troglodytes (chimpanzee) ORGANISM Pan troglodytes (chimpanzee) CRGANISM Pan troglodytes (chimpanzee) CRGANISM Pan troglodytes (chimpanzee) ACCACACACACACACACACACACACACACACACACACA | - | AUTHORS Green, E.D. TITLE Direct Submission JOURNAL Grovemont Circle, Gaithersburg, MD 20877, USA COMMENT On Nov 22, 2002 this sequence version replaced gi:22218452. Center: NIH Intramural Sequencing Center Center: NIH Intramural Sequencing Center Center: NIH Intramural Sequencing Center Contact: nisc_zoo@nhgri.nih.gov Contact: nisc_zoo@nhgri.nih.gov Contact: nisc_zoo@nhgri.nih.gov Contact: nisc_zoo@nhgri.nih.gov Center project Information Center project name: dhz Center clone name: 355A20 The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contigh has been established using one or more of the following: read-pair |
|--|---|---|--|
| | 954 GGAGGCGAGGTTGCAGTGGGCCGAGATCACATCACCGCCCTCCAGCCTGGGCGACAGAG 1013 111111111111111111111111111111 | 1194 TCCAGAGAGATAGAAAGAGGGGAGACAGAGAGAACAGAGAACAGAGAGAACACAGAGAACAGAGAACAGAGAACAGAGAACAGAGAACAGAGAACAGAGAACAGAGAACAGAGAACAGAGAACAGAGAACAGAGAACAG | 1430 TAGCCGAGGGAGAACCACAGAGAGATGGAAGAAGACTCTGAGAAAAAACCCAGAGACAAAG 11111111111111111 |

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* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.

* 28307 28406: contig of 28306 bp in length 28407 37956: contig of 9450 bp in length 37957 73522: contig of 9450 bp in length 73523: gap of unknown length 73523 73522: contig of 9945 bp in length 88367: contig of 9945 bp in length 73628 83567: contig of 9945 bp in length 88368 88817: contig of 5150 bp in length 88368 88818 88917: gap of unknown length
clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least BX average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                       Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 196656 bases at least Q40
Consensus quality: 197883 bases at least Q40
Consensus quality: 197883 bases at least Q20
Insert size: 215000, agarose-fp
Insert size: 199602; sun-of-contigs
Quality coverage: 9.03x in Q20 bases; sum-of-contigs
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unknown length
of 34168 bp in length
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193344: contig of 6862 bp in length
193444: gap of unknown length
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199463: gap of unknown length
200792: contig of 1329 bp in length.
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//note="assembly_fragment"
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//note="assembly_fragment"
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125712. .159879
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                                                                                                                                                                                                                                                                                             61.4%; Score 1227.2; DB 2; Length 200792; llarity 95.5%; Pred. No. 3.4e-292; Conservative 0; Mismatches 18; Indels 45; Gi
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Matches 1323; Conserv
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**Consists of 12 contigs. Gaps between the contigs.

**are represented as runs of N. The order of the pieces
**1s believed to be correct as given, however the sizes
**of the gaps between them are based on estimates that have
**provided by the submittor.
**This sequence will be replaced
** by the finished sequence as soon as it is available and
**the accession number will be preserved.

**Social Seconting of 6526 pp in length
** 6627 18812: contig of 6526 pp in length
** 6627 18813: contig of 12186 bp in length
** 6637 18813: contig of 12186 bp in length
** 61781 61780: contig of 42868 bp in length
** 61781 61780: contig of 35188 bp in length
** 61781 61780: contig of 35188 bp in length
** 61881 97068: contig of 3038 bp in length
** 97169 125206: contig of 2038 bp in length
** 125207 125306: gap of unknown length
** 125307 127021: contig of 1715 bp in length
** 127021: contig of 1715 bp in length
** 127021: 20387: contig of 2266 bp in length
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Submitted (08-AUG-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 176647)
                                                                                                 Sequencing Center, 8717
                                                                                             Submitted (14-NOV-2002) NIH Intramural Sequencing Center, 8 Grovemont Circle, Gaithersburg, MD 20877, USA On Nov 14, 2002 this sequence version replaced gi:22138439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently
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unknown length
of 6365 bp in length.
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                                                                                                                                                                                                                 Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                        Contact: nisc_zoo@nhgri.nih.gov
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Center clone name: 421P03
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                                                                               Direct Submission
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                                                             Green, E.D.
                                        REFERENCE
AUTHORS
    JOURNAL
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                                                                               TITLE
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E 1 (bases 1 to 17647)

S Akhter, N. Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Carlaga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J.,
Haghlghi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E.,
Laric, P., Lee-Lin, S.-G., Legaspi, R., Maduro, O.L., Maduro, V.B.,
Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J.,
Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A.,
Reddix-Dugue, N., Schandler, K., Schueler, M.G., Sison, C.,
Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L.,
Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D.
  1574
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                                                                                                                                                                                                                                                                                                CTGGCCTGGCTTCCGGAGACCCCTCCCCATTCTCCGGGCCAGGGAGGTAGGGAGTGACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     1815 AACTCAGGCCCGGTGCCCAGAGCCCAGGAGGCAGTGGCCAGGAAGGCACAGGCCTGA
                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC130188
AC130188.2 GI:24960890
HTG; HTGS_PHASE2; HTGS_DRAFT.
Papio anubis (olive baboon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 176647)
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 1076 TATCT---AAAAAAAAAAAGCTGTCAACAAATAGAGCAGAAGTGAAATAAAGGAAAATAA
                                           1193 ATCACAGAGGCATAGAAAGAC----AGGGAAGAACAGGGAGACAGAAACACCTGTGGCCC
                                                                                                    AATGAGCAAAATGCAGAGAAGAAAGCAAGCAATCCAGGCGCCAAGAATAGTGACCCAGAG
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Pred. No. 4.1e-236;
0; Mismatches 120; Indels
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44141 c 43622 g 43773 t
                   /organism="Papio anubis"
/mol_type="genomic DNA"
/db_xref="taxon:9555"
/clone="RP41-421P3"
/clone="RP41-421P3"
/1. 6526
                                                                                                                      6627. _18812
/note="assembly_fragment"
18913. _61780
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170283. .176647
/note="assembly_fragment
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Location/Qualifiers
                                                                                                clone_end:SP6
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88.0%;
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/note="single stranded/single chemistry region"
8265. 9528
/note="single stranded/single chemistry region"
                                                                                                              /note="single clone coverage"
5432. .5518
/note="single stranded/single chemistry region"
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note="single stranded/single chemistry region"
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replace="A"
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'note="delted in clone: XX-540F24"
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/replace=""
15447. 15448
/note="deleted in clone: XX-1Bcos"
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/note="deleted in clone: XX-1Bcos"
/replace=""
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.266. .5317
hote-"low quality region"
.266. .5317
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1766. 11880
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                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                              Submitted (26-NOV-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany 3 (bases 1 to 32799)
Lagemann, D. and Platzer, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                       Submitted (07-MAY-1997) Genome Analysis, Institute Of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany (bases 1 to 32799)
Lagemann, D. and Platzer, M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center clone name: Xx-540F24

Sequencing vector: PUC18; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 32765 bases at least Q40
Consensus quality: 32770 bases at least Q30
Consensus quality: 32770 bases at least Q30
Consensus quality: 32770 bases at least Q20
Quality coverage:13.12x
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//note="single stranded/single chemistry region"
2913. .2927
3166. .3173
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note="single stranded/single chemistry region"
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/note="single stranded/single chemistry region"
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                                                                                                                     Rump, A., Rosenthal, A., Drescher, B. and Schattevoy, R. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://genome.imb-jena.de/
Contact: gscj-submit@genome.imb-jena.de
------ Project Information
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/note="single clone coverage"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="X"
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/clone="XX-B6cos"
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                           Homo sapiens (human)
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| Oy 625 TGGGATTACAGGCGTGAGCCACGGCCGGCCATGATCATCTTGACTATGCTGATG 684 | | 805 CAGGAGTTTGGGCCACCACGAGGTGAAACTCTGTCTTACTAAAAAAAA | Db 5890Aatatachalattagcredgegegegegegegegegegegegegegegegegegeg | 1045 AACGAACAAGAGAAGAAGAAGAAGAAGAAGAAGAAAAAAA | 1165 ATCATTCAGAACCTTTAAAAAGAAGAAGAATCACAGAGGCATAGAAAGACAGGGAGGAACA | OY 1284 AGGAGAGAGAGAGAGAGAGAGACAGACAGAGAAAAAGACAG | 1403 CGAGATATTGAGAGACTCAGAAAGATAGCCGAGGGAGAACCACAGAGAGTTGAGAGAGA | OY 1583 CCAGAGTTGGTGAGAGCCAGATCTTAAGGCTGGGGAGGGA |
|---|----------|--|--|--|--|---|--|---|
| <pre>variation 1548115483 /note="deleted in clone: XX-540F24" /replace="" variation 15888 /note="A substituted in clone: XX-540F24"</pre> | n clone: | clone: XX- | variation 16793 Anote="G substituted in clone: XX-540F24" Variation 16817 Anote="C substituted in clone: XX-540F24" Variation 17129 Anote="C substituted in clone: XX-540F24" Anote="C substituted in clone: XX-540F24" Anote="C substituted in clone: XX-540F24" | variation //1489 // note="C substituted in clone: XX-540F24" // note="C substituted in clone: XX-540F24" // note="617" // note="single stranded/single chemistry region" // note="single stranded/si | /note="A substituted in clone: XX-540F24" /replace="G" /replace="G" /replace="G" /replace="G" /replace="A" /r | | | 505 CCGCCACTACGCCCGGCTAATTTTTTGTAGTAGAGACGGGGTTTCACCGTTTT 564 |

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Human DNA sequence from clone RPI-95C20 on chromosome Xpl1.3-11.4,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (Dases 1 to 138849)
McDougall, R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (05-MAR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 159, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Apr 18, 1998 this sequence version replaced g1:2222679.
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                                                                                                 GCCGGGATGCCCTCGATCTCCTGACCTCGTGATCCGCCCCGCCTCGGCCTCCCAAAGTGCT
                                                                                                                                                                                                                                                              GACAAGTACCTAAAGCCATCAGACTCTACCCTTTAAATATGCAGTTTGGGCCCAGGCACCG
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Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: humquery@sanger.ac.uk
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Z97181.1 GI:3059064
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Homo sapiens
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Consensus quality: 139579 bases at least Q40
Consensus quality: 140059 bases at least Q20
Consensus quality: 140054 bases at least Q20
Consensus quality: 140264 bases at least Q20
Estimated insert size: 140000; agarose-fp estimation
Estimated insert size: 141723; sum-of-contigs estimation
Quality coverage: 8.57 in Q20 bases; agarose-fp estimation

**NOTE: This is a "working draft' sequence. It currently

* consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                            Direct Submission
Submitted (09-FEB-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1197: gap of unknown length
18670: contig of 11473 bp in length
18770: gap of unknown length
141923: contig of 123153 bp in length.
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                                 9997.1 GI:18642721
HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
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Pred. No. 5.6e-102;
0; Mismatches 139;
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Center clone name: CITB-HI_207601
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                 Sequencing of Human Chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.jgi.doe.gov
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Center: Joint Genome Institute
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                                                                                                                                                          1 (bases 1 to 141923)
DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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al Similarity 79.0%;
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unordered pieces.
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Matches 573; Conserv
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CTGAGGCACGAGAGTCACTTGAACCCTGGAGGCGGAGGTTGCAGTGGGCCGAGATCACAT
      AAAAAAAAAAAAATCAGCCGGGTGTCGTGGGGCACACCTGTAATCCCCAGCTATGCTGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project Information
Center project name: chr-3
Center clone name: RP11-728B21 (bc0540)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Overlapping Sequences:
5': RP11-349E16 (UWGC:bc0646) AC098481
3': RP11-624D20 (UWGC:bc0494) AC068222
                                                                                                                                                                                                                             Contact: uwgchtgs@u.washington.edu
Drafting Center: BCM
                                                                                                                                                                                                         1047 CGAACAAGCAGTITGITGIACCTIAGITATA 1077
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Haugen, E.D.
Direct Submission
Unpublished
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ACCESSION
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JOURNAL
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSROT; Tr:, TREMBL; WP:, WORNPEP; Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122058 GTTCACGCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCGCCCCACCATC 121999
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                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/HGP/Chrx
RRD-95C20 is from the library RRCI-1 constructed by the group
Pieter de Jong, For further details see
http://www.chori.org/bacpac/home.htm
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Pred. No. 1.4e-101;
0; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /map="p11.3-11.4"
/clone="RP1-95C20"
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                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /chromosome="X"
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Local Similarity 77.6%;
les 583; Conservative
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PRI 01-JUN-2002
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1 (bases 1 to 171697)
1 (bases 1 to 171697)
1 (kaul, R.K., Olson, W.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-MAR-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA (bases 1 to 171697)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (01-JUN-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Jun 1, 2002 this sequence version replaced gi:19352302.
Homo sapiens chromosome 3 clone RP11-728B21, complete sequence. Ac114876.2 GI:21306686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: unknown; 53% of reads
Sequencing vector: plasmid; 47% of reads
Sequencing vector: plasmid; L08752; 0% of reads
Sequencing vector: plasmid; L08752; 0% of reads
Chemistry: Dye-terminator E1; 89% of reads
Chemistry: Dye-terminator Big Dye; 11% of reads
Assembly program: Phrap; version 0.990319
Consenus quality: 171547 bases at least Q30
Consensus quality: 171691 bases at least Q30
Consensus quality: 171697 bases at least Q30
Insert size: 171697; sum-of-contigs
Quality coverage: 9.2x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: University of Washington Genome Center
Center: University of Washington Genome Center
Center Code: UWGO
Web site: http://www.genome.washington.edu
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Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
Direct Submission
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| 9112 2380 2380 2713 930 | 4650 | 1662 | 6133 | 1897 | 4394 | 6941 | 1783 | 24086 | | | | | | | | | | | | | | | | | | | | | | |
|--|---|--|---|--|--|--|---|--|--|------|--------------------|------|-----------|---------------|----------|----------|------------|-----------|-----------|----------|------------|-----------|---|------------|-----------|-------------|-----------|---------|-----------|-------------|
| | 4641 | 1708 | 6082 | 1904 | 4433 | 6851 | 1799 | 23885 | | | | | | | | | | | | | | | | | | | | | | |
| 4508 1054 3396 1054 | 3122 | <800 | 4687 | <800 | 5041 | 2421 | 1314 | 3122 | 7057 | 1054 | 2421 | 1646 | 2867 | 6048 | <800 | 6386 | 008> | 3396 | 3950 | 2029 | 3630 | 3229 | | 500 | <800 | <800 | <800 | 1314 | <800 | <800 |
| 4492 1092 3332 1123 1803 | 3041 | 192 | 4763 | 587 | 5086 | 2278 | 1336 | 3223 | 7004 | 1 | 2341 | 1649 | 2822 | 6084 | 163 | 9648 | 311 | 9775 | 3900 | 2035 | 3012 | 5005 | # 1 0 0 0 1 1 0 0 0 1 1 1 1 1 1 1 1 1 1 | | 637 | 259 | 97 | 1242 | 270 | 23 |
| <pre><800 2308 1180 3831</pre> | 3300 | <800 | 4173 | 895 | 3963 | 4378 | 3831 | 2005 | 4173 | 2308 | 9989 | 3063 | 9989 | 810 | 4378 | 6032 | | | | | | | | | | | | | | |
| 360 | 3248 | 399 | 4134 | 006 | 3852 | 4463 | 3959 | 1990 | 4272 | 2327 | 6858 | 3056 | 6815 | 608 | 4433 | 6135 | | | | | | | | | | | | | | |
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| zero. from the | noted: .th an e., Phred | lencing were | digest. | Digest | rigest red digest below. | insert and reular BAC. | 400-800 bp) | epancies v ordered | James de la company de la comp | | FngrPrnt | -090 | 008 > | 3464 | <800 | 930 | 4873 | 3709 | 5487 | <800 | 13066 | 8687 | 5681 | 2844 | 10593 | 11745 | 8687 | | 6724 | 13754 |
| ce quality program. ed to quality zero. ave less than ally visible from the e as part | ss otherwise noted: sequenced with an lity data (i.e., Phred | Olve all sequencing; all regions were | y restriction digest. | ole Complete Digest | processing the state of the sta | ists of both insert and the entire circular BAC. | approximately 400-800 bp) | maining discrepancies | racs: Olityacif Oliceled | | Sequermap rngrPrnt | 2000 | | | | | 4919 4873 | | | 555 <800 | | | | | . 00 | 11874 11745 | | | 6660 6724 | 13999 13754 |
| th'sequence quality assembly program. been reduced to quality zero. scted to have less than not generally visible from the available as part | llows unless otherwise noted: randed or sequenced with an / high quality data (i.e., Phred | ide to resolve all sequencing d repeats; all regions were | onfirmed by restriction digest. | by Multiple Complete Digest | of fragmentally derived digest | nence consists of both insert and represent the entire circular BAC. | cutoff (approximately 400-800 bp) | ificant remaining discrepancies | ed lines. | | Sequermap | | 0 0 | 3403 | | | | | | t | | 8640 | | 42 | . 00 | 74 | | | | |
| ed with sequence quarter assembly prograve been reduced to expected to have lare not generally trare available as | nished as follows unless otherwise noted: ner double-stranded or sequenced with an or covered by high quality data (i.e., Phred | pressions and repeats; all regions were not | sembly was confirmed by restriction digest. | sen validated by Multiple Complete Digest | parison of the experimentally derived digest ence-predicted fragments is given below. | digested sequence consists of both insert and accurately represent the entire circular BAC. | bw a variable cutoff (approximately 400-800 bp) the fineerprint and hence do not appear | are no significant remaining discrepancies | ated by dashed lines. | | | 9098 | 6450 6 | <800 3403 | 334 | 951 | 4919 | 3694 | 5455 | 555 | 13221 | 8640 | 5654 | 2842 | 10800 | 11874 | 8529 | 286 | 0999 | 13999 |
| ed with sequence quarter assembly prograve been reduced to expected to have lare not generally trare available as | This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred | <pre>quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subvione or more than one M13</pre> | and the assembly was confirmed by restriction digest. | Sequence Validation: This sequence has been validated by Multiple Complete Digest | fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. | conically-digested sequence consists of both insert and order to accurately represent the entire circular BAC. | gments below a variable cutoff (approximately 400-800 bp) | ble. There are no significant remaining discreptions is experimental and predicted values. In impose ordered | in the captainments and products, only of the contracted by dashed lines. | | rngrkrnt sequermap | | 6382 6450 | 512 <800 3403 | <800 334 | 7924 951 | 10372 4919 | <800 3694 | 1054 5455 | 2867 555 | 1521 13221 | 9389 8640 | 3015 5654 | 10372 2842 | 883 10800 | 1054 11874 | 1314 8529 | 883 286 | 4687 6660 | 7564 13999 |

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This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered
                                                                                                                         Box 352145, Seattle, WA 98195, USA
3 (Dases I to 227137)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality -= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                            and Haugen, E.D.
Direct Submission
Submitted (15-JUN-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Jun 15, 2002 this sequence version replaced gi:16328287.
                                                                                                       Submitted (23-OCT-2001) Genome Center, University of Washington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SeqDerMap FngrPrnt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5': RP11-728B21 (UWGC:bc0540) AC114876, 123790-bp overlap 3': RP11-286L5 (UWGC:bc0344) AC103559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality coverage: 8.0x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100% of reads
reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: plasmid; L08752; 100% of read Chemistry: Dye-terminator ET; 76% of reads Chemistry: Dye-terminator B19 Dye; 24% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 227162 bases at least Q40 Consensus quality: 227131 bases at least Q30 Consensus quality: 227137 bases at least Q30 Insert size: 227137; sum-of contigs
                                                                                                                                                                                                                                                                                                                        Center: University of Washington Genome Center
                                                            Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
Direct Submission
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Center project name: chr-3
Center clone name: RP11-349E16 (bc0646)
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                                                                                                                                                                                                                                                                                                                                                                                                           Contact: uwgchtgs@u.washington.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----- Summary Statistics
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                                          (bases 1 to 227137)
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                                                                                                                                                                                                                                                                                                                                                                     Center Code: UWGC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 227137)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenplimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
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                                                                                                                                  CTCCCGGGTTCACGCCATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAGGCGCCC
                                                                                                                                                                                                                                                                                                 CGCCACTACGCCCGGCTAATTTTTTTTTTTTTTTTAGTAGACGGGGTTTCACCGTTTTA
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                                                                 Gaps
                                                              13;
                    Length 171697;
                                                            Indels
                                          Pred. No. 1.4e-101;
0; Mismatches 140;
                    DB 9; L
1.4e-101;
                    Score 455;
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| 61 <800 44 <800 7321 7358 | 1886 1877 23 | 6367 6431 1 | 4192 4145 3577 3633 5827 5912 | 17721 17419 303 <800 3 | 7973 7948 2574 2596 9 | 395 <800 | 2993 3003 2820 2850 7814 7838 | 646 <800 9069 9045 1345 1327 | 3887 1553 1517 | <800 1792 1741 2723 2 | 2008 7744 7870 1059 | 1000 | 0000 F000 F0000 F0 | 40/1 40/1 4010 | | 7070 | 5405 | 1/19 1081 2054 3054 3054 3054 3054 3054 3054 3054 3 | 11000 | 111111111111111111111111111111111111111 | Match 22.8%; Score 455; DB 9; Length 227137; | 572; Conservative 0; Mismat | 326 GGTGGTGTCTATGATCATCTTTTTTTTTTTTTTTTTTTT | 91443 GARGGITCATITCCTCAGGITTITITITTTTTTTTTTTTTTTT | 386 CTCGCTCTGTCGCCCCAGCTCGAGTGCAGTGGCGGGATCTCGGCTCACTGCAAGCTCCGC 445 | 91503 CTTGCTCTGTGGCCCAGGTGGGAGTGCAGTGGCGCAATCTCGGCTCACTGCAAGCTCCGC 91562 | 446 CTCCGGGGTTCACGCCATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAGGCGCC 505 | 91563 CTCCCAGGTTCACGCCATTCTCCTGCCTCAGCCTCCGAGTAGGTGGGACTACAGGCGCC 91622 | 506 CGCCACTACGCCCGGCTAATTTTTGTATTTTTAGTAGACGCGGTTTCACCGTTTTA 565 | 91623 CGCCACCACGCCCGGCTAATTTTTTGTATTTTTAGTAGACGGGGTTTCACCGTGTTA 91682 | 566 GCCGGGATGGCCTCGACCTCGTGATCCGCCCCCCCCTCGGCCTCCCAAAGTGCT 625 | 91683 GCCAGGATGTCTCGATCTCCTGACTCGTCGCCCCCGCCTCGGCCTCCCAAAGTGCT 91742 | 626 GGGATTACAGGCGTGAGCCACCGCGCCGGCCATGATCTTCTTGACTATGCTGATGT 685 | 91743 GGGATTACAAGCGTGAGCCACCGCGCCCGGCC-TCCTCAGGTTTTTATTAAACCAGTGAA 91801 | 686 GACAAGTACCTAAAGCCATCAGACTCTACCCTTTAAATATGCAGTTTGGGCCAGGCACG 745 | 91802 GCTCATCTAATGAAGGAAATTATGACAGGGTGTTAAAAACTAGGCAGGGGATGGGCATGA 91861 |
|---------------------------|--------------|-------------|-------------------------------|------------------------|-----------------------|----------|-------------------------------|------------------------------|----------------|-----------------------|---------------------|-------|--|--------------------|-------|-------|-------|---|-------|---|--|-----------------------------|---|---|--|--|--|---|--|---|--|--|--|--|---|--|
| | | | | | | | | | | | | | | | | | ٠ | | | | Query Match | Matches | Oy | qa | Qy | QQ | Qy | QQ | | οp | Qy | QΩ | Qy | QQ | QY | ΩD |
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| 3196 | 6483 | 008 | <800 | 1367 | 1684 | 2357 | 866 | 7067 | 3196 | 1327 | 2251 | 5023 | <800 | 4697 | <800 | 16792 | 3013 | 1813 | 1011 | 3382 | 1011 | 4528 | 7668 | 4697 | 832 | 1327 | 866 | 922 | 10357 | 2846 | 9439 | 1526 | 2775 | 1071 | <800 | 10357 |
| 3211 | 6382 | 715 | 944 | D | 1649 | 2341 | 971 | 7003 | 3223 | 1336 | 2278 | 5086 | | 4763 | | 16514 | 3041 | 1803 | 1123 | 3332 | 1092 | 4492 | 7571 | 4767 | 817 | 1340 | 1004 | 891 | 10593 | 2970 | 9418 | 1527 | 2795 | 1052 | 305 | 10618 |
| 8633 | <800 | 46/1 | 937 | 70/7 | 2141 | 2346 | 9731 | 13681 | 6723 | <800 | 8633 | 11716 | 10477 | 2850 | 5704 | 8633 | 12924 | <800 | 5489 | 3751 | 4887 | 937 | <800 | 3506 | 3633 | 2850 | 3909 | 5704 | <800 | <800 | <800 | 7870 | <800 | <800 | 3909 | 3369 |
| 9698 | 9 | 4641 | 924 | 6007 | 9877 | 2356 | 9092 | 13999 | 0999 | 286 | 8529 | 11874 | 10800 | 2842 | 5654 | 8640 | 13221 | 555 | 5455 | 3694 | | 951 | 334 | 3403 | 3587 | 2819 | 3838 | 5684 | 373 | 63 | 203 | 7896 | 332 | 407 | 3904 | 3318 |
| 22843 | 7368 | 1186 | 1681 | 6090 | 43/6 | 5251 | 2380 | 4145 | 2088 | 1416 | 8730 | 1416 | 3003 | 1088 | 9934 | 7368 | 2380 | 4786 | 1186 | 2689 | 1186 | <800 | 750 | 1681 | 1877 | 1490 | 1350 | 5251 | <800 | 1681 | 1877 | 1416 | <800 | 5251 | 3262 | 7368 |
| 22527 | 7364 | 1250 | 1646 | 7000 | 4415 | 5203 | 2339 | 4104 | 2067 | 1413 | 8832 | 1451 | 3108 | 1155 | 10132 | 7178 | 2392 | 4819 | 1188 | 2666 | 1188 | 4 . | 732 | 1680 | 1855 | 1537 | 1361 | 5212 | 24 | 1608 | 1731 | 1439 | 327 | 5312 | 3221 | 7582 |

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91969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (04-NOV-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 4 (bases 1 to 119147) Waterston, R.H.
                                                                                                                                                                                                                                                                   PRI 09-MAR-2002
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AAAAAAAAAAATCAGCCGGTGTCGTGGGGCACACCTGTAATCCCAGCTATGCTGGAG 925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (09-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Feb. 21, 2002 this sequence version replaced gi:18042516.
                                                                                              91922 CGGAGTTCGAGACCAGTCTGGCCAACGTGTCAAAACCCCATCTCTACT-----
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens BAC clone RP11-793H20 from 4, complete sequence. AC098873 AC036224 G1:18855169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (21-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MpG 93108, USA
5 (bases 1 to 119147)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Waligorski,J., Haakenson,W. and Spalding,L.
The sequence of Homo sapiens BAC clone RP11-793H20
Thopublished (2001)
3 (bases 1 to 119147)
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Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Sulston, J.E. and Waterston, R.
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746
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 0.0); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by otherwise noted: This sequence was finished as follows unless restriction digest.

MAPPING INFORMATION:

Louis Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-260K18, 2000 bp overlap; the clone sequenced to the right is RP11-473N2. Actual start of this clone is at base position 106515 of RP11-260K18; actual end is at base position 119147 of RP11-793H20.

Single plasmid region exists between 77265 and 77307. Polymorphisms exist between AC079118, AC024191 and AC098873.

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The sequence of AC036224 has been incorporated into AC098873
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4936. .5061
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4908. .4933
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30890 CTAAAATTTCCATATTTCCCTCAGATGGAAAAATGATAACACCAGTAGAAGTTTTAATAG 30949
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                                                                                                                                                                                           11010 GGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGCAAAGCTCTGTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   851 ACTAAAAAAAAAAAAAAAAAAAAAAAAATCAGCCGGGTGTCGTGGGGCACACCTGTAATC
                                                                                                                                                                            AAGCTCCGCCTCCCGGGTTCACGCCATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACT
                                                                                                                                                                                                                                                                                                                               617 CAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCATGATCTTCTTG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     791 GAATCACTTGAGGCCAGGAGTTTGAGACCAGCCTGGCCAACATGGTGAAACTCTGTTT
                                                                                                                                                     Gaps
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6e-101;
                                                                                                                                                   0; Mismatches 126;
                                                                                                                111arity 80.0%; Score 452.4; Conservative 0: Mismath
                                                                       /rpt_family="L1"
26252. .26537
/rpt_family="Alu"
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Best Local Similarity
Matches 589; Conserv
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18576. 18866
18867. 18866
18867. 19110
rpt_family="L1"
00551. 205051.
1762. 21530
1762-"match to EST AA774138 (NID:g2826027) ab68h06.rl"
1866. 21319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rpt_family="L1"
11350. .22285
note="CpG_island (%GC=69.3, o/e=0.90, #CpGs=92)"
1695. .21995
                                                                                                                                               /rpt_family-"MER1_type"
9143. 9317
/rpt_family-"MER1_type"
9465. 9696
/rpt_family-"MIR"
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23993. .24105
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22792. .23246
         7086. .7509
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23247. .23458
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16646, 16020
                                                                                                rpt_family="Alu"
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1206. .14500
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23575. .23961
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910

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/rpt_family="L1M4b"
complement(2472. .2666)
/rpt_family="L1MC/D"
2683. .2963
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                                                                                                                                                      COMMENT
                                                                                                                                                  Manmalia; Euthenia; Primates; Catarrhini; Hominidae; Homo.
Manmalia; Euthenia; Primates; Catarrhini; Hominidae; Homo.
Mazny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
Benton,J., Blurdett,C., Blankenburg,K., Bennin,D., Bouck,J.,
Burkett,C., Blurrell,K.L., Bylo,N.C., Carron,T.E.,
Grarter,M., Cavasos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Carter,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.R., Davis,C.,
Coyle,M.D., Dathorne,C., Harris,C., Edgar,D., Edwards,C.C.
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Frantz,P.,
Garza,N., Harris,C., Harris,R., Homai,F., Homai,F., Li,J., Li,Z., Lidhtarge,D., Hally,N., Lal,B., Lewis,L.,
Louiseged,H., Lozado,R.J., Lu,X., Lucier,R., Martindale,A.,
Martinez,E., Massey,E., Mawhiney,E., Mitchell,T., Mohabbat,R.,
Martinez,E., Massey,E., Mawhiney,E., Mitchell,T., Mohabbat,R.,
Martinez,E., Massey,R., Mawhiney,E., Mitchell,T., Mohabbat,R.,
Morgan,M., Okwonou,G., Oraqunye,N., Notedo,R., Parces,R., Parce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (23-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
9, Chases 1 to 108893)
Worley.K.C.
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                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostómi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AC079169.32 GI:21263154
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                              KEYWORDS
VERSION
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SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                          CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
Worley, K.C.

Direct Submission

Submitted (22-JAN-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

May 30, 2002 this sequence version replaced gi:21206031.

INFORMATION: http://www.hgsc.bcm.tmc.edu/oremail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found
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/note="overlaps bases 108750. .110816 of clone AC002404"
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complement(549. .580)
/rpt_family="LlM4"
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/organism="Homo sapiens"
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/rpt_family="Alusx"
complement(1760. .2236)
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/db_xref="taxon:9606"
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/rpt_family="L1M4"
1370. .1394
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| Db 50324 GAATGGTCTCGATCTCCTGATCCGCCCCCCCCCCCCCAAAGTGCTGGGA 50383 Qy | Qy 810 GTTTGAGACCAGCCTGGCCAACATGGTGAAACTCTTACTAAAAAAAA | 114 114 115M 115M 115M 115M 115M 115M 11 | TITLE DITECT SUBMISSION JURINE DITECT SUBMISSION JURINE DITECT SUBMISSION AUTHORS REFERENCE 3 (bases 1 to 100208) AUTHORS RAUL, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Buckley, D., Kibukawa, M., Raymond, C. and Haugen, E.D. TITLE Direct Submission JOURNAL SUBMISSION AUTHORS AUTHORS Saenphimmachak, C., Buckley, D., Kibukawa, M., Raymond, C. and REFERENCE 4 (bases 1 to 100208) AUTHORS RAUL, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Buckley, D., Kibukawa, M., Raymond, C. and Haugen, E.D. TITLE Direct Submission JOURNAL Submitted (17-MAY-2003) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA COMMENT On May 17, 2003 this sequence version replaced gi:25705321. Center University of Washington Genome Center Center Code: UNGC Web Site: http://www.genome.washington.edu |
|---|--|--|--|
| repeat_region 2564291 | | repeat_region /rpt_family="AluSx" repeat_region /rpt_family="AluSx" 6391.6656 /rpt_family="AluSx" 6585.6673.6677 /rpt_family="ITAAA)n" repeat_region /rpt_family="LimD3" 7076.7099 /rpt_family="LimD3" 7076.7099 /rpt_family="AluSx" 7076.7099 /rpt_family="AluSx" 7076.7099 /rpt_family="GAAAA)n" repeat_region /rpt_family="AluSx" repeat_region /rpt_family="AluSx" /rpt_family="AluSx" repeat_region /rpt_family="AluSx" /rpt_family="LTR40a" repeat_region complement(8778.8996) /rpt_family="LrR3" repeat_region complement(8778.3994) /rpt_family="LrR33" repeat_region complement(9197.9359) | Query Match 22.5%; Score 450.6; DB 9; Length 108893; Best Local Similarity 80.0%; Pred. No. 1.6e-100; Action 1.6e-100; Matches 572; Conservative 0; Mismatches 129; Indels 14; Gaps 3; Qy 330 GTGTCTATGATCTTTTTTTTTTTTTTTTTTTTTTTTTTT |

| 8217 8355 1084 1065 1752 1748 | 7535 7745 77 <800 1057 1047 | 477 <800 766 776 297 <800 | 5023 5020 619 <800 10235 10177 | 61 <800 1381 1379 1580 1550 | 4008 4017 459 <800 336 <800 | 1890 1924 1679 1655 2820 2839 | 5242 5141 2384 2388 3407 3423 | 846 843 1873 1835 5948 5883 | 3480 3460 1659 1655 835 854 | 823 843 4721 4758 603 <800 | 2118 2082 3389 3384 4462 4442 | 1996 1924 1331 1379 6616 6652 | 2474 2515 2045 2050 1944 1944 | 2746 2745 1252 1237 10220 10177 | 3321 3384 7959 7933 | 1441 1379 3562 3548 | 3094 3079 3091 3117 | 3442 3471 9174 9315 | 169 <800 5473 5486 | 1055 1065 445 <800 | 3927 3866 | 1288 1313 | 4579 4557 | 5480 5550 | 41 <800 | 5950 6031 | . 2655 2688 | 15 <800 | 213 <800 | 432 <800 | 008> 889 | 172 <800 | 73 <800 | 2709 2745 | Location/Qualifiers |
|-------------------------------|---|--|---|---|--|--|--|---|-----------------------------|--|--|-------------------------------|---|---------------------------------|---|---|--|---|---|--|---|--|--|--|----------------------------------|-----------|---------------------------------|-----------------------------------|---|---------------|--|----------|-------------------------|--------------------|-------------------------------|
| - | | | | | 4 | 1 | | | | | | | 7 | | | | | | | | | | | | | | | | | | | | | | FEATURES source |
| Drafting Center: SC | Center project name: chr-1 Center clone name: sc0392 | sc0392 was derived from the original BAC (RP11-298P9). using yeast homologous Gapture technique. | Sequencing vector: plasmid; 53% of reads Commandary vector: valenid; 33% of reads | Sequenting Vector, prasmin, 2007/2; 47% Of reads Chemistry: Dye-terminator Rap Dye; 100% of reads Assembly program: praction 0 000310 | Consensus quality: 100206 bases at least Q40 | Consensus quality: 100208 bases at least 020 Tonors of 100208 bases at least 020 | Quality coverage: 25.1x in Q20 bases; sum-of-contigs | Overlapping Sequences: 5': RP11-297123 (UWGC:sc0384) AC098656. 3777-hn overlan | h | Sequence Quality Assessment: This entry has been annotated with sequence quality | estimates computed by the Phrap assembly program. All manually edited bases have been reduced to mality zero | | Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part | | This sequence was finished as follows unless otherwise noted: | alternate chemistry or covered by high quality data (i.e., Phred cumplity >= 30: an attemnt was made to resolve all commendate. | problems, such as compressions and repeats; all regions were | covered by at least one plasmid succione of more than one Mis subclone, and the assembly was confirmed by restriction digest. | Sequence Validation: This secure has been well-dated by Weltiele Comment to Discret | fings-printing. Comparison of the experimentally derived digest frammants with seminance-predicted frammants with seminance-predicted frammants with seminance-predicted frammants is digns bolow. | The electronically-digested sequence consists of both insert and vertor, in order to accurately represent the entire structure. | Small fragments below a variable cutoff (approximately 400-800 bp) | in the table. There are no significant remaining discrepancies between the experimental and predicted values instance. | fragments are separated by dashed lines. Hindlil | drPrnt SeaberMap FnarPrnt Seaber | | 27861 27870 2775 2822 4460 4442 | 10835 10615 15690 15691 2067 2066 | CONTRACTOR CONTRACT | ALL COOL COOL | 114.0 COO COO COO COO COO COO COO COO COO CO | 0000 | 1,004/ 41/0 4218 3336 3 | 7338 5633 5550 859 | 818 843 4670 4557 24 <800 |

Rouse, G., Wu, Z., Kibukawa, M., Raymond, C.

and

Raymond, C., Clendenning, J., Ivey, R.G.

Center, University of USA

Rouse, G., Wu, Z., Kibukawa, M., Raymond, C.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 182569) Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C
                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (31-MAY-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On May 31, 2002 this sequence version replaced g1:14702054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: Mi3; LOBB21; 468 of reads Sequencing vector: plasmid; LOBF35; 548 of reads Chemistry: Dye-terminator ET; 368 of reads Chemistry: Dye-terminator ET; 368 of reads Chemistry: Dye-terminator ET; 368 of reads Chemistry: Dye-terminator Big Dye; 598 of reads Assembly program: Phrap; version 0.990319 Consensus quality: 182255 bases at least Q40 Consensus quality: 182559 bases at least Q30 Consensus quality: 182559 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 182569; sum-of-contigs
Quality coverage: 7.6x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                          Center: University of Washington Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.genome.washington.edu
Contact: uwgchtgs@u.washington.edu
Drafting Center: BCM
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                                                                                                                                                                                                                                                                                       Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A.,
Saenphimmachak, C., Phelps, K.A., Buckley, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: chr-3
Center clone name: RP11-111P21 (bc0233)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------ Project Information
                                                                                                                                                                                                                                      Submitted (12-JUL-2001) Genome
Box 352145, Seattle, WA 98195,
3 (bases 1 to 182569)
                                                                                                                                                                 2 (bases 1 to 182569)
Kaul, R.K., Olson, M.V.,
Haugen, E.D.
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 Homo sapiens (human)
                                                                                                                                      Direct Submission
                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                           Hangen, E.D.
                                                                                                                                                    Unpublished
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SOURCE
ORGANISM
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REFERENCE
AUTHORS
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20265 c 19464 g 29311 t
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fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and
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1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence has been validated by Multiple Complete Digest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence Validation:
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182569 bp DNA linear PRI 31-MAY-2002 AC092500 AC063916 AC092500 AC063916 HTG.

ACCESSION VERSION KEYWORDS DEFINITION

AC092500 LOCUS

25534-bp overlap

| 954 896 2367 2378 703 <800 2319 2351 1845 1824 16180 15729 13494 13082 1386 1444 6022 5991 6106 6034 6231 6411 7893 7834 | <800 2770 2813 2111 | 2351 1437 1444 311 | 896 1306 1312 4499 | 7463 6844 6845 52 | 10022 2198 2185 3595 | 250 201 6701 926 | 11268 11268 11268 1 | 1312 3058 | 01/C 6T5C | 1312 5087 541 | 1296Z 756Z | FEATURES Location/Qualifiers source 1182569 | /organism="Homo sapiens" /mol_type="genomic DNA" | /db_xret="taxon:9606" /chromosome="3" //limesome="3" | 06673 | DASE COUNT 54/30 d 598/1 C 5///8 g 50130 L ORIGIN | Query Match 22.5%; Score 450; DB 9; Length 182569; | Hest Local Similarity 80.5%; Fred. No. 2.5e-100; Matches 566; Conservative 0; Mismatches 125; Indels 11; Gaps 3; | Qy 351 TTTTTTTTTTTTTTTTTTTTGAGACGAGTCTCGCTCGCCCAGGCTGGAGT 410 | Db 36794 TIGITITITITITITITITITITIGAGACGAGATCICGCTCTGTCGCCCAGGCTGGAGT 36853 | 411 GCAGTGGCGGATCTCGGCTCACTGCAAGCTCCCGGGTTCACGCCATTCTCCTG | Db 36854 GCAGTGGCGGGATCTCGGCTCACTGCAAGCTCCGCGTCCCGGGTTCACGCCATTCTCCTG 36913 | 36914 CCTCAGCCTACCAAGTAGCTGGGACTACAGGCGCCCGCCACTACGCCCGGCTAATTTTT | Qy 531 TGTATTTTAGTAGAGACGGGGTTTCACCGTTTTAGCCGGGATGGCCTCGATCTCCTGAC 590 | Db 36974 GTATTTTAGTAGAGATGGGGGTTTCACCGTTTTAGCCGGGATGGTCTCCATCTCTGAC 37033 | Qy 591 CTCGTGATCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCG 650 | Db 37034 CTCGTGATCCGCCCACCTCCGAAGTGCTGGGATTACAGGCGTGAGCCACCGCG 37093 | CCCGGCCATGATCATCTTGACTATGCTGATGAGAAGTACCTAAAGCCATCAGACT 710 | Db 37094 CCTGGCCGAAACAGCATTTTTTTTTTTCCCCTAGGTTGATGGTTCTGAAAATCACTTTTA 37153 | QY 711 CTACCCTTTAAATATGCAGTTTGGGCCAGGCACCGTGGCTCATGCCTGTAATTCCAGCAC 770 |
|--|---------------------|--------------------|--------------------|-------------------|----------------------|------------------|---------------------|-----------|-----------|---------------|------------|---|---|--|-------|---|--|---|---|--|---|---|---|--|---|---|--|---|---|---|
| ular BAC. 100-800 bp) sear ancies ordered | FngrPrnt | 8539 | <800 | 1321 | <800 | 918 | 1805 | 3988 | 3041 | 6630 | 1131 | 6630 | 3041 | <800 | <800 | <800 | 5707 | 918 | 10825 | 1805 | 3988 | 7834 | 10825 | 1321 | 8539 | 19330 | 736 | 1936 | 5991 | 1501 |
| ire ci nately not a discr niquel | SeqDerMap Fr | 9698 | 9 | 1332 | 375 | 891 | 1804 | 3923 | 2990 | 6498 | 1141 | 6574 | 3033 | 140 | 59 | 140 | 5413 | 925 | 11072 | 1799 | 4025 | 7257 | 10884 | 1340 | 8413 | 18710 | 760 | 1951 | 5919 | 1538 |
| epresent the cutoff (approved to the cutoff (approved to the cutoff (approved to the cutoff the cut | FngrPrnt | 8420 | 2185 | 4821 | 1012 | 8420 | 008> | 846 | 6845 | 7149 | <800 | 3700 | <800 | 6411 | 1444 | 9480 | 4653 | 2185 | 920 | 1312 | 11997 | 6411 14593 | <800 | <800 | 2813 | <800 | 8420 | 3453 | 4394 | 2185 |
| in order to accurately represent the entragments below a variable cutoff (approxinatesolute) in the fingerprint and hence do table. There are no significant remaining the experimental and predicted values. Units are separated by dashed lines. | SeqDerMap | 8212 | 2067 | 4790 | 1012 | 8184 | 446 | 837 | 6762 | 7177 | 612 | 3808 | 361 | 6436 | 1475 | 9769 | 4733 | 2135 | 930 | 1292 | 11292 | 14482 | 656 | 490 | 2794 | 125 | 8400 | 3534 | 4480 | 2214 |
| Ocr, in order to accu- I fragments below a not resolved in the he table. There are een the experimental ments are separated Hindlil | FngrPrnt | 1754 | 6517 | <800 | <800 | 2351 | 968 | <800 | 8651 | 1604 | 3762 | 5056 | <800 | 8049 | 2091 | 6034 | 3149 | 10022 | 10022 | <800 | 6517 | 968 | 2091 | 4472 | 1460 | <800 | 7463 | 4006 | 17700 | <800 |
| vector, in Small fragi are not res in the tab between the fragments fragments | SeqDerMap | 1769 | 6382 | 512 | 449 | 2329 | 864 | 86 | 9282 | 1607 | 3752 | 5118 | 281 | 7991 | 2048 | 5856 | 3137 | 10058 | 10112. | 682 | 6527 | 212 | 2126 | 4504 | 1479 | 266 | 7408 | 4055 | 17535 | 52 |

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| | 10 | 410.4 | 20.5 | | 22 | AAL03692 AAL05001 | Human reproductive |
| | 12 | 406.2 | 20.3 | 12970 | 23 | ABL97894 | testicular |
| O | 13 | 406 | 20.3 | | 22 | AAK89986 ABA18400 | Human digestive sy |
| υ | 15 | 405.8 | 20.3 | | 22 | AAS40516 | DNA encoding human |
| O | 16 | 405.8 | 20.3 | | 22 | AAL04142 AAK67282 | Human reproductive |
| υ | 18 | 403.6 | 20.2 | | 24 | ABT00010 | n neuregulin |
| O | 19 | 403.6 | 20.2 | | 24 | ABT01503 | Human neuregulin 1 |
| ט ט | 21 | 403.6 | 20.2 | , | 2 6 | AAK96733 | neuregulin |
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| (| 53 | 401.8 | 20.1 | | 22 | ABA18399 | Human nervous syst |
| ບ | 25 | 401.8 | 20.1 | | 7 7 7 | AAS4 USI 3 AALO4 139 | DNA encourng numan Human reproductive |
| O | 56 | 401.6 | 20.1 | | 22 | AAF97870 | Human neuroblastom |
| U | 27 | 401.6 | 20.1 | | 22 | AAF97871 | Human neuroblastom |
| | 53 | 400.6 | 20.0 | | 22 | AAK8200/ AAK82008 | Human immune/haema |
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| טנ | 7 6 | 398.4 | ν. α. α. | | 77 | AAK86336 AAK70780 | Human immune/haema Human immune/haema |
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                                                            AGAGGTGGTGAATCACTTGAGGCCAGGAGTTTGAGACCAGCCTGGCCAACATGGTGAAA
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                                                                                                                                                                                                                                                                                                                                            Indels
                              New kallikrein-like (KLK-L) proteins for diagnosing and protein mediated disorders, especially cancer.
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                                                                                                                                                                                                                                                                                                           100.0%; Score 2000;
llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                                                        Claim 1; Page 143-149; 184pp; English.
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Matches 2000; Conserv
AAB21296
                                                                                                                                                                                                                                                                                 Sequence 11570
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The present genomic sequence is that of human pituitary adenylate cyclase estivating polypetide (PACAP). This gene is localised to the short arm of chromosome 18p11 and synthesised in the retinal ganglion cells. The genomic DNA is isolated from lymphocytes of individuals. The coding
                                                                                                                                                                                                                                                                                                                            Pituitary adenylate cyclase activating polypeptide; PACAP gene; probe; neuropsychiatric disorder; bipolar affective disorder; BAD; BP-I; UTR; severe bipolar affective disorder; schizoaffective disorder manic type; SAD-W; chromosome 18pil; retinal ganglion cell; STS marker; ADCYAPI; dinucleotide repeat polymorphism marker; W3440; detection; mutation; clinical observation; subjective report; compound; mapping; diagnosis;
AGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCCCACCCCTGG
                                                                                      a dinucleotide repeat polymorphism an STS marker, ADCYAP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of a chromosome associated willy for diagnosis of bi-polar
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affective disorder and schizoaffective disorder manic type
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/*tag= b
/product= "PACAP protein"
/note= "Includes exons and introns"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
72668..72991
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72993..77243
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marker, W3440 and
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                                                                                                                                                                                                                             DNA; 84607
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                                                                                                                                                                                                                                                                                                       Human PACAP genomic sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of a gene linked to the neuropsychiatric disorders,
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                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                            AAX90847 standard;
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region of the gene has a dinucleotide repeat polymorphism marker known as W3440 and an STS marker, ADCYAP1 is located in the 3'UTR. These markers are useful to map the gene physically and genetically to the chromosome 18. This sequence can be used to design probes for detecting the presence or absence of a mutation in the wild type PACAP gene. It is also useful for genetic diagnosis of neuropsychiatric disorders like bipolar affective disorder [BP-1] and schizoaffective disorder manic type (SAD-M), which are more valid than current clinical diagnosis based on clinical observation and subjective reports. It is used for identifying compounds that modulate PACAP gene expression which are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20438 TGTGCCTATTTTGGTTTAACTTCTTATTTTGAGTTTTTTGGATACAACTAGAACAAGCAC
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                                                                                                                                                                                                                                                   55; Gaps
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                                                                                                                                                                                                                    Score 424.4; DB 20;
Pred. No. 1.4e-65;
                                                                                                                                                                                                                                   Pred. No. 1.4e-65;
0; Mismatches 146;
                                                                                                                                                       treatment of PACAP disorders.
                                                                                                                                                                                                                   Query Match 21.2%;
Best Local Similarity 75.4%;
Matches 617; Conservative
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The invention relates to detecting (MI) granulocyte (GC) activation CG (GCA), by detecting the level of expression of gene(s) (GS) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated the expression level to an expression of GS is indicative of GCA.

Also included are modulating (M2) GA by contacting of with an agent capable of modulating GCA or an inflammation (especially for an agent capable of modulating GCA or an inflammation (especially chronic) in a fissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the correction of a subject to a pathogen or sterile inflammatory disease, by detecting the correction of expression in a sample of the tissue of gene(s) from GS, where correcting (M5) an inflammation of especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation, or in a tissue, an allergic response of gene(s) from GS, where correcting (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. M1 is useful for a creening a gene or sterile of modulating GCA m3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile correcting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile or response in a subject or a pathogen or sterile or response in a subject or a pathogen or sterile or response in a subject or a pathogen or sterile or response in a subject or a pathogen or sterile or response in a subject or a pathogen or sterile or response in a subject or a pathogen or sterile or response in a subject or a pathogen or steril
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                              Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                             Human cDNA differentially expressed in granulocytic cells #133.
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                         ABK83562 standard; cDNA; 139904 BP
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                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                772 TTGGGAGGCAGAGGTGGGTGAATCACTTGAGGCCAGGAGTTTGAGACCAGCCTGGCCAAC
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parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                     Gaps
                                                                                                                                                                   Length 139904;
                                                                                                                               Sequence 139904 BP; 39268 A; 29759 C; 30173 G; 40704 T; 0 other;
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                                                                                                                                                                                                  0; Mismatches 129; Indels
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                                                                                                                                                                   DB 24;
                                                                                                                                                                   Score 416.6; DB 2
Pred. No. 3.4e-64;
                                                                                                      ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                   Query Match 20.8%;
Best Local Similarity 79.1%;
Matches 551; Conservative
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Cardiovascular system antigen; human; mouse; rabbit; goat; horse; cat; chicken; sheep; immunosuppressive; antiarthritic; vasotropic; dog; antirhoulumatic; antiproliferative; cardiant, neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperpoliferative disorder; breast; liver; cardiovascular disorder; ds; cerebrovascular disorder; nervous system disorder; bacterial infection; fungal infection; viral infection; ocular disorder; endocrine disorder; wound healing; skin aging; organ transplantation; tissue regeneration; anti-infertility.
                                                                                                                                         2000US-0179065.
2000US-0180628.
2000US-0184664.
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2000US-0189874.
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05-SEP-2000;
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                                                                                   Homo sapiens
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17-MAR-2000;
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15449 CACCCGGCC----GATGTTTGCAACTCTTTAACAGTGAAAACAAATCCCAGCTTTTA-- 15501
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                                                                                                                                                                                                                                                                                                                                                                      1561 GTGGTGCACACACTGTAATCCCACCTACTTGGGAGGCTGAAGCACGAGAATCACTTGA
                                           709 CICIACCCITIAAAIAIGCAGTIIGGGCCCAGGCACCGIGGCICAIGCCIGIAAIICCAGC
                                                                                 -----TAAAATATATAAGCTGGGCTGGCCGGTGGCTCACACCTGTAATCCCAGC
                                                                                                                      ACTITGGGAGGCAGAGGTGGGTGAATCACTTGAGGCCAGGAGTTTGAGACCAGCCTGGCC
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02-MAR - 2000;
17-MAR - 2000;
11-MAR - 2000;
19-MAY - 2000;
07-JUN - 2000;
28-JUN - 2000;
07-JUL - 2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     the cardiovascular system antigen polypeptides of the invention.

Cardiovascular system antigen polypeptides of the invention.

Cardiovascular system antigen and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by actecting the presence or absence of a mutation in a cardiovascular system antigen polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cerebral isohaemia, nervous system disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fungl, ocular disorders such as corneal infection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as premature labour and infertility, as offenced or an easier of sease, renal disorders such as pleurisy. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15329 TTTGTATTTTTAGTAGAGGGGTTTTGCCGTGTTAGCCCAGGATGGTCTCGATCTCCTG 15388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transplantation, to regenerate tissues and in chemotaxis.
Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349 TITITITITITITITITITITITITITITITITICAGACGGAGICICGCICIGICGCCCAGGCIGGA
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                                                                                                                                                                                                                                                                                                                              New cardiovascular system related polynucleotides and polypeptides, useful for diagnosing, treating and/or preventing disorders of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 20.8%; Score 415.2; DB 22; Length 17397; Best Local Similarity 78.6%; Pred. No. 5e-64; Matches 558; Conservative 0; Mismatches 123; Indels 29; (
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                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 1945; 674pp; English.
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05-DEC-2000; 2000US-0251988.
05-DEC-2000; 2000US-0256719.
06-DEC-2000; 2000US-0251479.
08-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251899.
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05-JAN-2001; 2001US-0259678.
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14-AUG-2000; 2000US-0225270.
14-AUG-2000; 2000US-0225757.
14-AUG-2000; 2000US-0225757.
14-AUG-2000; 2000US-0225759.
18-AUG-2000; 2000US-0225759.
18-AUG-2000; 2000US-0225759.
22-AUG-2000; 2000US-0225759.
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2000US-0246476.
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(HUMA-) HUMAN GENOME SCI INC

Ruben SM; Rosen CA, Barash SC,

WPI; 2001-451930/48.

New cardiovascular system related polynucleotides and polypeptides, useful for diagnosing, treating and/or preventing disorders of the cardiovascular system -

Claim 1; SEQ ID No 1943; 674pp; English.

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Sequences AAS35741-AAS36942 represent genomic DNA molecules, which encode the cardiovascular system antigen polypeptides of the invention. Cardiovascular system antigens and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in a cardiovascular system antigen polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cerebral ischaemia, nervous system disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fungi, ocular disorders such as corneal

horse;

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Cardiovascular system antigen; human; mouse; rabbit; goat;
 ------TAAAATATAAGCTGGGCTGGGCGGGGGCTCACACCTGTAATCCCAGC, 15545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15546 AGTTTGGGAGGCCAAGGCAGGTGGATCACTTGAGCTCGGGTGTTCAAGACCAGCTTGGCC 15605
                                                                                                                                                                                                                       15143 TGTTCGTAACTCTTTTTGTTGTTGTTAAGACAGACTCTTGCTCTGTCGCCCAGGCTGGA 15202
                                                                                                                                                                                                                                                                                                                            15263 TGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCACCCGCCACCAAGCCCGGCTAA-TTT 15321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15606 AACATGGTAAAACGCTGTCTTTACT------AAAAATACAAAATTAGCCAGGT 15653
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         gastrointestinal disorders such as Crohn's disease, renal disorders such as a glomerulonephritis and respiratory disorders such as asthma and pleurisy. The polypeptides can also be used to aid wound healing, to prevent skin ading due to sunburn, to maintain organs before transplantation, to regenerate tissues and in chemotaxis.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fitp.wipo.int/pub/published_pct_sequences.
endocrine disorders such as premature labour and infertility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15442 CACCCGGCC----GATGTTTGCAACTCTTTAACAGTGAAAACAAATCCCAGCTTTTA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               709 CTCTACCCTTTAAATATGCAGTTTGGGCCAGGCACGGTGGCTCATGCCTGTAATTCCAGC
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Pred. No. 5.1e-64;
0; Mismatches 123; Indels 29; (
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78.6%;
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Matches 558; Conservative
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chicken; sheep; immunosuppressive; antiarthritic; vasorropic; dog; antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; neoropic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; described; cerebrovascular disorder; nervous system disorder; bacterial infection; fungal infection; viral infection; ocular disorder; endocrine disorder; gastrointestinal disorder; renal disorder; respiratory disorder; wound healing; skin aging; organ transplantation; tissue regeneration;
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2000US-0180628.
2000US-0184664.
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07-JUN-2000;
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23-AUG-2000;
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PR 14-SEP-2000 2000US-022339.
PR 14-SEP-2000 2000US-0232399.
PR 14-SEP-2000 2000US-0232399.
PR 14-SEP-2000 2000US-0232399.
PR 14-SEP-2000 2000US-0232390.
PR 14-SEP-2000 2000US-0233063.
PR 14-SEP-2000 2000US-0233064.
PR 25-SEP-2000 2000US-0233063.
PR 25-SEP-2000 2000US-0233063.
PR 26-SEP-2000 2000US-0244061.
PR 26-SEP-2000 2000US-0244617.
PR 26-SEP-2000 2000US-0244921.
PR 26-SEP-2000 2000US-024921.
PR 26-SEP-2000 20
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Sequences AAS35741-AAS36942 represent genomic DNA molecules, which encode the cardiovascular system antigen polypeptides of the invention. Cardiovascular system antigens and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in a cardiovascular system antigen polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cerebral ischemia, nervous system disorders such as Alzheimmer's disease, infections caused by bacteria, viruses and fungi, ocular disorders such as corneal infection, endocrine disorders such as premature labour and infertility,
                                                                                                                                                                                                                                                                                                                                                                             New cardiovascular system related polynucleotides and polypeptides, useful for diagnosing, treating and/or preventing disorders of the
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                                    . 2000US-0256719.
2000US-0251479.
2000US-0251856.
2000US-0251868.
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2000US-0251990.
2000US-0254097.
2001US-0259678.
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  2000US-0251030
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05-JAN-2001;
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409 GTGCAGTGGCGGGATCTCGGCTCACTGCAAGCTCCGGCCTCCCGGGTTCACGCCATTCTCC

15151 TGTTCGTAACTCTTTTTTGTTGTTGTTAAGACAGACTCTTGCTCTGTCGCCCAGGCTGGA 15210

349 TITITITITITITITITITITITITITITITIGAGACGGAGTCTCGCTCTGTCGCCCAGGCTGGA

Score 415.2; DB 22; Length 19345; Pred. No. 5.1e-64; 0; Mismatches 123; Indels 29; Gaps

Query Match 20.8%; Best Local Similarity 78.6%; Matches 558; Conservative C 408

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529 TTTGTATTTTAGTAGAGGGGGTTTCACCGTTTTAGCCGGGATGGCCTCGATCTCCTG

589 ACCTCGTGATCCGCCCCCCCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCG

649 CGCCCGGCCATGATCATCTTCTTGACTATGCTGATGTGACAAGTACCTAAAGCCATCAGA 708

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2000US-0228924
2000US-0229287
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08-SEP-2000;
12-SEP-2000;
14-SEP-2000;
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08-NOV-2000;
15503 -----TABABATATATAAGCTGGGCTGGGCGCGGTCACACACGTGTAATCCCAGC 15553
                                                                      ACCCTGGAGGCGGAGGTTGCAGTGGGCCGAGATCACATCACCGCCCTCCAGCCTGGGCGA 1008
                                                            828
                                                                                               Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
                                                            769 ACTITIGGGAGGCAGAGGTGGGTGAATCACTTGAGGCCAGGAGTTTGAGACCAGCCTGGCC
                          CTCTACCCTTTAAATATGCAGTTTGGGCCAGGCACCGTGGCTCATGCCTGTAATTCCAGC
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ID AAL05001 standard; DNA; 12970 BP
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16-MAR-2000;
17-MAR-2000;
18-APR-2000;
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07-JUN-2000;
28-JUN-2000;
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14-AUG-2000;
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                                                                                                     6059 CTCCCGAGTAGCTGGGACTACAGGCGCCTGCCACCATGCCCGGCTAATTTTT--TATTT
                                                      6001 TIAGTAGACACAGGGTTTCACCGTGTTAGCCAGGATGGTCTCCATCTCCTGACCTCTGA
                                                                                                                                                                                                                                                         5711 GAAACCCTGTCTCTACTAAAAAT-----ATAAAAATTAGCCATGCTGAC
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                                                                                                                                                                       ATGA-TCATCTTCTTGACTATGCTGATGTGACAAGTACCTAAAGCCATCAGACTCTACCC
                                                                                                                                                                                                      5881 ACCACTCAGTGTTTTTAAATGGGTAAAATATTTGTACAGATACTTAACAAAC----
                                                                                                                                                                                                                                     717 TTTAAATATGCAGTTTGGGCCAGGCACCGTGGCTCATGCCTGTAATTCCAGCACTTTGGG
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ID ABL97894 standard; DNA; 12970
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2000US-0180628.
2000US-0184664.
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04-FEB-2000;
24-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6179 TITITITITITITITITITEAGACGGAGTCTTCCACTGTCGCCCCAGGCTGGAGTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12970 BP; 3310 A; 2917 C; 2938 G; 3805 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 414.8; DB 22; Lews-Pred. No. 5.8e-64;
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al Similarity 73.3%;
608; Conservative
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
17-NOV-2000;
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01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
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08-DEC-2000;
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2000US-0217496
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       17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
                                                                    4 - AUG - 2000;
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02-OCT-2000;
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08-NOV-2000; 17-NOV-2000; 17-NOV-2000;

Ruben SM; (HUMA-) HUMAN GENOME SCI INC Rosen CA, Barash SC,

WPI; 2001-483232/52.

Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer

Disclosure; SEQ ID NO 2546; 766pp; English.

The present invention provides the protein and coding sequences of 973

ABK94412;

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6002
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               sequences can be used in the treatment of cardiovascular, urinary syst reproductive system immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding protein fragment of the invention.
                                                                                                                                                                                               358 TITITITITITITITITITITIGAGACGGAGTCTCGCTCTGTCGCCCCAGGCTGGAGTGCAGTGG
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   human testicular antigens, and fragments of their genomic sequences.
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                                                                                                                                     DB 23; Length 12970;
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                                                                                                      Sequence 12970 BP; 3310 A; 2917 C; 2938 G; 3805 T; 0 other;
                                                                                                                                                                0; Mismatches 197; Indels
                                                                                                                                    Score 414.8; DB 2
Pred. No. 5.8e-64;
                                                                                                                                 20.7%;
                                                                                                                                                                608; Conservative
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ABK94412 standard; DNA; 74037 BP.

ABK94412/c RESULT

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pharmaceutical composition for treating a cardiovascular disease such as coronary heart disease, hypertension, atherosclerosis, or related to coronary angiogenesis or fatty acid metabolism e.g. diabetes and familial hypercholesterolaemia. The gene or a polynuclectide fragment of the EDN/ECE/EDNR signaling system are useful as forensic markers, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the gene encoding EDN. ECE or EDNR (II) or a vector (III) expressing (IV) or (III) is useful for producing cells capable of expressing a molecular variant polypeptide which is associated with a cardiovascular disease. (II), (III), the EDN. ECE or EDNR polypeptide, or a cell expressing a molecular variant gene comprising (I) is useful for identifying and obtaining a pro-drug or drug capable of modulating the activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system or its gene product, or for identifying and obtaining an inhibitor of signaling system or its gene product. The isolated proteins and polypeptide of the EDN/EDNR/ECE signaling system or its gene product. The isolated proteins and polypeptide of the EDN/EDNR/ECE signaling system or its gene product. The isolated proteins and polypeptide of the EDN/EDNR/ECE polynucleotides encoding them are useful for preparation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes a polynucleotide (I) of the endothelin (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR) signaling system which is associated with a cardiovascular disease. (I),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or
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                                                                                                                                                        endothelin receptor; signaling system; cardiovascular disease; coronary heart disease; hypertension; atherosclerosis; anglogenesis; fatty acid metabolism; diabetes; familial hypercholesterolaemia; forensic marker; transgenic animal; solid support; SNR; cardiovascular regulator; gene; ds; single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for
                                                                                                                                                                                                                                                                                                                                                                                                                                              "Single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enzyme/receptors of endothelin and endothelin converting enzyme signaling system associated with cardiovascular disease, useful
                                                                                                                                                                                                                                                                                                                                                                                     "Single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Single nucleotide polymorphism"
                                                                                                                                       endothelin converting enzyme 1; ECE 1; EDNR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotide of the endothelin/endothelin converting
                                                                                                 DNA encoding endothelin converting enzyme 1 (ECE-1) #2.
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                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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replace(8938,T)
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                                                         (first entry)
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                                                                                                                                       Endothelin; EDN;
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                                                                                                                                                                                                                                                                                 Homo sapiens
                                                         27-AUG-2002
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2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0189374.
2000US-0199076.
              WO200155320-A2
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05-SEP-2000;
05-SEP-2000;
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08-SEP-2000;
12-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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08-SEP-2000;
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08-SEP-2000;
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14-SEP-2000;
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06-SEP-2000;
                                                                 17-JAN-2001;
                                                                                                                                                                                    19-MAY-2000;
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                                                                                                                                                                                                                                                                                                    22531 TCTTTTTTTTTTTTTTTTTTTTTTTTTGAGGGAGTCTCGCTCTGTTGCCCAGGCT 22472
                                                                                                                                                                                                                                                                                                                                                                                                                     22231 CTGCGCCCGGCCCTTTTTTTTTTTAAGGAAAATGGAAACTATTCATTTTTTTGAAATAA, 22172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                  465
                                                                                                                                                                                                                                                                                                                                                                                           646 CCGCGCCCGGCCATCATCTTCTTGATGTGATGTGACAAGT-----ACCTAA 698
                                                                                                                                                                                                                                      TITITIGIALTTITAGIAGAGACGGGITITCACCGITITIAGCCGGGAIGGCCTCGAICTC 585
                                                                                                                                                                                                                                                                                                                                                                                                                                            699 AGCCATCAGACTCTACCCTTTAAATATGCAGTTTGGGCCAGGCACCGTGGCTCATGCCTG 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGTCACTTGAACCCTGGAGGCGGAGGTTGCAGTGGGCCCAGATCACATCACCGCCCTCC 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reproductive system related antigen; reproductive system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    879 TCAGCCGGGTGTCGTGGGGCACACCT-GTAATCCCAGCTATGCTGGAGGCTGAGGCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAATTCCAGCACTTTGGGAGGCAGAGGTGGATCACTTGAGGCCAGGAGTTTGAGAC
cardioavscular regulator Endothelin converting enzyme 1 (ECE-1). Note: This sequence does not appear in the specification but has been obtained from GenBank using information given in the invention.
                                                                                                                                346 TCTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGACGGAGTCTCGCTCTGTCGCCCAGGCT
                                                                                                                                                                                 406 GGAGTGCAGTGGCGGGATCTCGGCTCACTGCAAGCTCCGCCTCCCGGGTTCACGCCATTC
                                                                             Score 414.6; DB 24; Length 74037;
Pred. No. 7.2e-64;
0; Mismatches 144; Indels 19; Gaps
                                                                                                                                             21882 AGCCTGAGGGACAGATTGAGACCCTGTCTCAAAAAACAACAACAACAACAAAA 21830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 74037 BP; 18330 A; 19332 C; 19180 G; 17195 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human reproductive system related antigen DNA SEQ ID NO: 6380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAL03692 standard; DNA; 10445
                                                                             20.78;
77.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                             Query Match 20.7
Best Local Similarity 77.1
Matches 550; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer; gene therapy; ds
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Ruben SM

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The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
                       Isolated nucleic acid molecule encoding a reproductive system antigen
                              is used in preventing, treating or ameliorating a medical condition
                                        Disclosure; SEQ ID NO 6380; 1297pp + Sequence Listing; English.
Rosen CA, Barash SC,
            WPI; 2001-465570/50
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20000S-0241809.
20000S-0241826.
20000S-0244617.
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                                                                                                                                                                                                                                                                                                                                                               2000US-0251988
                      29-SEP-2000;
29-SEP-2000;
02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
                                                                                20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
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20-OCT-2000;
01-NOV-2000;
08-NOV-2000;
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8686
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                                                                                                                        418
                                                                                                                                                                                                             478
                                                                                                                                                                                                                                                                                                538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8687 GCTATCTGGCTCACTGCAAGCTCTGCCTCCCGGGTTCACGCCATTCTCCTGCCTCAGTC
                                                                                                                                                                                                                                                                                                                     9036 GCCGGGTGGGCAGATTACCTGGGGTCAGGAGTTCAAGACCAGCCTGGTCAACATGGTGA
                                                                                                                                                                                                                                                                                                                                                                                539 TAGTAGAGACGGGGTTTCACCGTTTTAGCCGGGATGGCCTCGATCTCCTGACCTCGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     719 TAAATATGCAGTTTGGGCCAGGCACCGTGGCTCATGCCTGTAATTCCAGCACTTTGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8977 AAAATAAGAAATTTAGGCCTGGCGTGGTGGCTCAAGCCTGTAATCTCAGCA-TTTGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        899 ACACCTGTAATCCCAGCTATGCTGGAGGCTGAGGCACGAGATCACTTGAACCCTGGAGG
                                                                                                                            359 TTTTTTTTTTTTTTTTGAGACGGAGTCTCGCTCTGTCGCCCAGGCTGGAGTGCAGTGGC
                                                                                                                                                                                                             419 GGGATCTCGGCTCACTGCAAGCTCCGCCTCCCGGGTTCACGCCATTCTCCTGCCTCAGCC
                                                                                                                                                                                                                                                                                                8926 AGAATCTGCATTTTAAAAAATCCCCAGTTCTAAGTACAGGGGCATCTTAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        779 GCAGAGGTGGGTGAATCACTTGAGGCCAGGAGTTTGAGACCAGCCTGGCCAACATGGTGA
                                                                                  24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 410.4; DB 22; Length 10445; Pred. No. 3.4e-63; 0; Mismatches 126; Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1017 GACTCTGTCTCAAATAAATAAATAAACAAACGAACAAGCAGTTTGTTGTA 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10445 BP; 2469 A; 2885 C; 2678 G; 2413 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAL05001 standard; DNA; 12970 BP
                                       20.5%;
78.9%;
                                       Query Match 20.5
Best Local Similarity 78.9
Matches 560; Conservative
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AAL05001
ID AAL05
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Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
                                                                                        Human reproductive system related antigen DNA SEQ ID NO: 7689.
                                                                                                                                                                                                                                                                                                                                                         17-JAN-2001; 2001WO-US01339
                                            21-NOV-2001 (first entry)
                                                                                                                                                                                                                                                             WO200155320-A2.
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14-SEP-2000;
                                                                                                                                                                                                                                                                                                            02-AUG-2001
AAL05001;
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6135
                                                                                                                         testicular antigen; testes; cancer; metastasis; immune disorder;
1002 TGGGCGACAGGCAAGAÇTCTGTCTCAAATAAATAAATAAACAAACGAACAAGCAGTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reproductive system disorder; urinary system disorder; gene therapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human testicular antigen encoding DNA fragment SEQ ID NO: 2546
                                                                                                                                                                        1062 ITGTACCTTAGTTATATCTAAAAA 1086
                                                                                                                                                                                                                         6196 TTGAGTTGTAGGAATTGCTTATATA 6220
                                                                                                                                                                                                                                                                                                                                                ABL97894 standard; DNA; 12970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAR-2000;
18-APR-2000;
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14 - AUG - 2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                   ABL97894;
                                                                                                                                                                                                                                                                                                    RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6016 GCCGGGCATGGTGGCAGGCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAAT 6075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         942 CACTIGAACCCTGGAGGCGGAGGTTGCAGTGGGCCGAGATCACATCACCGCCCTCCAGCC 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3910 TCCCAGAACTTTGGGAGGCCGAGGCGAGCAGATCAA--GAGGTCAGGAGATGGAGACCAT 5967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342 ATCTTCTTTTTTTTTTTTTTTTTTTTTTTTGAGACGGAGTCTCGCTTGTCGCCCA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               402 GGCTGGAGTGCCGGGATCTCGGCTCACTGCAAGCTCCGCCTCCCGGGTTCACGCC 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAATTTTTTTTTTTTTTTTAGTAGAGGGGGTTTCACCGTTTTAGCCGGGATGGCCTCGA 581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of a number of human reproductive system related antiqens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5797 GCCACCGCGCCTGGCCCGGCCCACATATTTTCGTTTAAGTATCTGTACAAATATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     762 ITCCAGCACTTTGGGAGGCAGAGGTGGTGAATCACTTGAGGCCAGGAGTTTGAGACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              582 TCTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCACCGCCCCGGCCATGATCATCTTCTTGACTATGCTGATGTGACAAGTACCTAAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   702 CATCAGACTCTACCCTTTAAATATGCAGTTTGGGCCAGGCACCGTGGCTCATGCCTGTAA
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                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAGGCGCCCCGCCACTACGCCCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 20.3%; Score 406.2; DB 22; Length 12970; Best Local Similarity 75.7%; Pred. No. 1.9e-62; Matches 564; Conservative 0; Mismatches 158; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 7689; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12970 BP; 3310 A; 2917 C; 2938 G; 3805 T; 0 other;
                                                                                                                                                                                                                                                                          Ruben SM;
                  08-DEC-2000; 2000US-0251856.

08-DEC-2000; 2000US-0251868.

08-DEC-2000; 2000US-0251869.

08-DEC-2000; 2000US-0251999.

11-DEC-2000; 2000US-0251990.

11-DEC-2000; 2000US-0254097.
                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
2000US-0251479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein of the invention.
                                                                                                                                                                                                                                                                       Barash SC,
                                                                                                                                                                                                                                                                                                                   WPI; 2001-465570/50
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2000US-0232397.
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20-OCT-2000;
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20-OCT-2000;
01-NOV-2000;
08-NOV-2000;
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5499 ATTITCITIGGITITITGGITTTTTTTTTTTTTGAGATGGAGTCTCGCTCTGTCGCCCA 5558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer
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2000US-0249244.
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2000US-0249265.
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05-DEC-2000;
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14-Aug-2000; 2000us-0225213.
14-Aug-2000; 2000us-0225214.
14-Aug-2000; 2000us-0225214.
14-Aug-2000; 2000us-0225266.
14-Aug-2000; 2000us-0225267.
14-Aug-2000; 2000us-0225267.
14-Aug-2000; 2000us-0225267.
14-Aug-2000; 2000us-0225267.
14-Aug-2000; 2000us-0225275.
14-Aug-2000; 2000us-0225758.
14-Aug-2000; 2000us-0225758.
14-Aug-2000; 2000us-0225758.
14-Aug-2000; 2000us-0225758.
14-Aug-2000; 2000us-0225758.
14-Aug-2000; 2000us-0225776.
15-EP-2000; 2000us-0229345.
01-SEP-2000; 2000us-0229345.
02-SEP-2000; 2000us-0233399.
14-SEP-2000; 2000
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08-NOV-2000;
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chronic colitis;
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                                                                                                                                                                                                                                                         6016 GCCGGGCATGGTGGCAGGCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAT
                                 702 CATCAGACTCTACCCTTTAAATATGCAGTTTGGGCCAGGCACCGTGGCTCATGCCTGTAA
                                                        TTCCAGCACTTTGGGAGGCAGAGGTGGGTGAATCACTTGAGGCCAGGAGTTTGAGACCAG
                                                                                                                                                                                                                                                                                                         942 CACTTGAACCCTGGAGGCGGAGGTTGCAGTGGGCCCAGATCACATCACCGCCCTCCAGCC
                                                                                                                                                                                                                                      882 GCCGGGTGTCGTGGGGCACACCTGTAATCCCAGCTATGCTGGAGGCTGAGGCACGAGAGT
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ulcerative colitis; infection; Hirschsprung's disease;
digestive system disorder; Meckel's diverticulum; ds.
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2000US-0198123.
2000US-0205515.
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2000US-0214886.
2000US-0215135.
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2000US-0224519
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17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
30-JUN-2000;
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24-FEB-2000;
02-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                710 TCTACCCTTTAAATATGCAGTTTGGGCCAGGCACCGTGGCTCATGCCTGTAATTCCAGCA
                                                                                                                                                                                                                                                                                                                                                                    770 CTTTGGGAGGCAGAGGTGGGTGAATCACTTGAGGCCAGGAGTTTGAGACCAGCCTGGCCA
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                                                             CCTCGTGATCCGCCCCCCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGĊ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of digestive system, particularly cancer and cancer metastases -
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16-MAR-2000;
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19-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
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Ruben SM 20000S-0241787. 2000US-0241808. 2000US-0241809. 2000US-0241826. 2000US-024221. 2000US-024617. 2000US-0246475. 2000US-0246476. 2000US-0246477. 2000US-0246523. 2000US-0246524. 2000US-0246525. 2000US-0246526. 2000US-0246527. 2000US-0246527. 2000US-0246527. 2000US-0246527. 2000US-0246611 2000US-0246613 2000US-0249208 2000US-0249209 2000US-0249210 2000US-0249211 2000US-0249211 2000US-0249212 2000US-0249213 2000US-0249213 2000US-0249213 2000US-0249213 2000US-0249217 2000US-0249218 2000US-0249244 2000US-0249245 2000US-0249265 2000US-0249265 2000US-0249265 2000US-0249297 2000US-02492997 2000US-02492997 2000US-0251030 2000US-0251988 2000US-0256719 2000US-0251879 2000US-0251856 2000US-0251869 (HUMA-) HUMAN GENOME SCI INC 2000US-0250391 2000US-0251160 Rosen CA, Barash SC, 20-0CT-2000; 20-0C 17-NOV-2000; 2 17-NOV-2000; 2 17-NOV-2000; 2 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 05-JAN-2001;

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system , cancers and metastases -

WPI; 2001-541565/60.

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1341 AGGCTGCAGTGAGCC--GATCACACCACTGCACTCCAGCCTGGACAACAGAGTGAGACTC 1398
                                                                                                                                                                                                                                          Human; prostate cancer antigen; cytostatic; uropathic; diagnositc;
reproductive system; chromosomal marker; forensic; urinary disorder;
chronic nephritis; blood-related disorder; thrombosis; ds.
                                                                                                                                                                                                               DNA encoding human prostate cancer antigen, Seq ID No 668.
                          AAS40516 standard; DNA; 4433 BP
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2000US-0184664
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                                                                                                                                                          The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune hamolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections.
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Disclosure; SEQ ID NO 10731; .1701pp + Sequence Listing; English.
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Pred. No. 2e-62;
0; Mismatches 167; Indels 21;
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Best Local Similarity 74.8%;
Matches 557; Conservative (
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The invention relates to novel isolated human prostate cancer antigen polynocleotides (I) and polypeptides (II). (I) and (II) are useful for preventing, treating or ameliorating a medical condition when administered. (I). (II) and the antibody to (II) are useful for treating, preventing and/ or prognosting disorders related to the reproductive system including prostate cancers; urinary disorders e.g. chronic nephritis; and blood-related disorders e.g. thrombosis. (II) can be used for testing and detection e.g. as a chromosomal marker and in forensics. (I) and the anti-(II) antibody can be used in testing and detection in immunoassays. AAS40061-AAS4075 represent the human prostate cancer antigen coding sequences, and related PCR primers and sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly.from WIPO at: ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the reproductive system including prostate and also for testing and detection e.g. diagnosis -
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             20000S - 024 926 7:
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Best Local Similarity 74.89
Matches 557; Conservative
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01-DEC-2000;
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|---|---|---|--|---|--|--|------------------------------------|---|
| 609 CGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCATGA | TCATCTTCTTGACTATGCTGATGTGACAAGTACCTAAAAGCCATCAGCCTTTAAA | ATATGCAGITIGGGCCAGGCACCTGGCTCATGCCTGTAATTCCAGCACTTTGGGAGGCA | GAGGTGGGTGAATCACTTGAGGCCAGGAGTTTGAGACCAGCCTGGCCAACATGGTGAAAC | TCTGTCTTTACTAAAAAAAAAAAAAAAAAAAATCAGCCGGGTGTCGTGGGGCACA | CCTGTAATCCCAGCTATGCTGGAGGCTGAGGCACGAGAGTCACTTGAACCCTGGAGGCGG | AGGTEGCAGTGGGCCGAGATCACATCACCGCCTCCAGCCTGGGCGACAGAAGCAAGACTC | | |
| JAGGCGTGAGCCACCGC | BACAAGTACCTAAAGCC TAGTCCCAGTATCAC | rGGCTCATGCCTGTAAT | AGGAGTTTGAGACCAGO | aaaaaaaaaaatcag aaaacgcaaaaatcag | GCTGAGGCACGAGAGTC | rcaccgccrccagccr | 1046 13011 | 55:15 |
| CGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCATGA | TTGACTATGCTGATGT | STTTGGGCCAGGCACCG | AGGTGGGTGAATCACTTGAGGCCAGGAGTTTGAGACCAGCCTGGCCAACAI | TACTAAAAAAAAAA TACT | CCCAGCTATGCTGGAGG | NGTGGCCGAGATCACAT | TGTCTCAAATAAATAAATAAACAAA 1046 | ist 5, 2003, 05:55:15 |
| CGGCCTCC | | ATATGCAG | GAGGTGGG AGGCGGG | TCTGTCTT 111 GCCATCTC | CCTGTAAT | | TGTCTCAP TGTCTCAP | Search completed: August Job time : 503.736 secs |
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Run on:

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AF101960 Luman Homo sapiens genomic clone pTWB59.14, genomic survey
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2971)
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Medicine and Radiology
Duke University Medical Center
Box 2610, MSRB, Room 117, Durham, NC 27710, USA
part of a 1.4 megabase contig including the LOH11A metastasis
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             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Minimum DB s Maximum DB s

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Searched:

Sednence:

BM701794 UI-E-CQ1-BM999040 UI-H-DIO-AQ748733 HS_5540_A BX352666 BX352666 AL573566 AL573566 BX482403 HOMO Sap1

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         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [dases 1 to 297]
Bepler, G. O'Briant, K.C., Kim, Y.C., Schreiber, G. and Pitterle, D.M. A 1.4-Mb high-resolution physical map and contig of chromosome segment 11p15.5 and genes in the LOHIIA metastasis suppressor
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Medicine and Radiology
Duke University Medical Center
Box 2510, MSRB, Room 117, Durham, NC 27710, Part of a 1.4 megabase contig including the
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/map="11p15.5"
/clone="pTWB59.14"
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Pred. No. 27;
0; Mismatches 119;
                   /organism="Homo sapiens"
mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="11p15.5"
/clone="pTWBS9.14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                            283 TITGTATITCCAGIAGAGAC--IGTITCACCAIGITGGGCCAGGCTGGTCTAGAACTCCTG
   GCACAGTGGCGTGATYTCAGCTCGCTGCAACCTCTGCCTCCCGTGTTCAAGCAATTYTCC
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
17El: 81-438-52-3975
Fax: 81-438-52-3986
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AL500585 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10 NORMALIZED HOmo sapiens cDNA clone CSODJ015YK20 3-PRIME, mRNA sequence.

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/clone="CSODJ015XK20"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
10-NORMALIZED"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8901.f For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=cSODJ015BF10NPl&cluster=8901.f. Contact
Feng Liang Email: fliang@lifetech.com/URL:
http://fulllength.invitrogen.com/InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: cSODJ015BF10NP1.
Location/Qualifiers
AGTCACTTGAACCCTGGAGGCGGAGGTTGCAGTGGGCCGAGATCACATCACCGCCCTCCA
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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/mol_type="mRNA"
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Clone distribution: MGC clone distribution information can.be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 43 Row: j Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                               Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
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                  Direct Submission
Submitted (25-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1058 AGTGCAGTGGCGTGATCTCAGCTCACTGCAAGCTCTGCCTCCTGGGTTCAGGCCATTCTC
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                                                                                                                                                                cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
/clone="TWAGE:5022014"
/tissue_type="wuscle, rhabdomyosarcoma"
/clone_lib="NIH MGC_17"
/lab_host="DH10B-R"
                                                                                                   http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pOTB7" 364 c 447 g
                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                    Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tch 16.9%;
al Similarity 75.3%;
500; Conservative C
                                                                                                    NIH-MGC Project URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .1641
                                                                                                                                                                                                                                   info@bcgsc.bc.ca
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JOURNAL
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     AUTHORS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1641)
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1. .652
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEMBB1000637"
/tissue_type="whole embryo, mainly body"
/dev_stage="embryo, 10 weeks"
/clone_lib="HEMBB1"
/note="Vector: pME18SFL3"
/note="Vector: pME18SFL3"
/note="Vector: pME18SFL3"
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Pred. No. 6.9e+02;
0; Mismatches 125;
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Homo sapiens, clone IMAGE:5022014, mRNA
BC033224
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Best Local Similarity 75.7'
Matches 494; Conservative
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01-H-DIO-avn-j-13-0-UI.s1 NCL_CGAP_DIO Homo sapiens cDNA clone
IMAGE:5881836 3', mRNA sequence.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                       2770 TITITITITITITITITITITITITITITITITITICGTAAGACGGAGTITIGCTCTGTCTCCCA
                                                                                                                                  522 TAATTTTTTTTTTTAGTAGAGGGGTTTCACCGTTTTAGCCGGGATGGCCTCGA
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                                                          402 GGCTGGAGTGCAGTGGCGGGATCTCGGCTCACTGCAAGCTCCGGCTTCCGGGTTCACGCC
                                                                                                                                                                          --- ATCATCTTCTTGACTATGCTGATGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                         689 AAGTACCTAAAGCCATCAGACTCTACCCTTTAAATATGCAGTT-TGGGCCAGGCACCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31;
                               Indels
Score 336; DB 11;
Pred. No. 2.4e+02;
); Mismatches 170;
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16.8%;
illarity 73.2%;
Conservative
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Homo sapiens
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  Query Match
Best Local Similarity
Matches 549; Conserv
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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BM999040
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HOMO sapiens, Similar to hypothetical protein FLJ20489, clone
BC036630
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                                                                                                                                                                                                                   AACCCTGGAGGCGGAGGTTGCAGTGGGCCGAGATCACATCACCGCCCTCCAGCCTGGGCG 1007
                709
                                                                                                    887
                                                                                                                               602
                                                                                                                                                           947
                                                                                                                                                                          827
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Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 2772)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (15-OCT-2002) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
 99009----
                                                                                                                                                          888 IGTCGTGGGGCACACCTGTAATCCCAGCTATGCTGGAGGCTGAGGCACGAGAGTCACTTG
                                         CACTITGGGAGGCAGAGGTGGGTGAATCACTTGAGGCCAGGAGTTTGAGACCAGCCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) &
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:5263792"
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/clone_lib="NHH_MGC_95"
/lab.ost="DH10B"
/note="Vector: pBluescript"
623 c 602 g 865 t
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCWNSFORT_6; 1st strand cDNA was primed
with a NotL-ollgo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoNY sites of the pCWNSFORT 6 vector.
Library was not normalized.

251 c 231 g 249 t 3 others
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                                                                                                                                                                                                                              343 TCTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGACGGAGTCTCGCTCTGTCGCCCAG 402
                                                                             415 CCCAGTACTICAGGAAGCCAAGGAGGTGGATTCTTTGAGCCCAGAAATTCGAGACCAGG 474
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  361 GAAGGACTGACGAGACTCACT-----GGTTGGCCGGGCGTGGTGACTCATATCTGAAAT 414
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 969)
                                                                                                                                                                                                                                                                                                                 TCCAGCACTTTGGGAGGCAGAGGTGGGTGAATCACTTGAGGCCAGGAGTTTGAGACCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ьты, Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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/clone="InAGE:58B1836"
/tissue_type="Lung Focal Fibrosis"
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/lab_bst="NBH10B"
/lab_bst="NBH10B"
/lab_bst="DH10B"
/lab_bst="DH10B"
/clone_lib="NCI_CGAP_DI0"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_l: EcoR I; Site_2: Not I;
/note_TGAP_DIO is a cDNA library containing the following tissue(s): A pool of Lung Focal Fibrosis. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first strand cDNA contains a library tag sequence that is located between the Not I site and the (GT)B tail. The sequence tag for this library is
  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
CLONE Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CLONE Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CLONE DIATE OF CONSTITUTION INFORMATION OF THE FOUND
The following repetitive elements were found in this CDNA
sequence: 11-315, >ALU (matched compliment) 386-662, >ALU
POLYA-Yes.
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TAG_TISSUE-lung with fibrosis
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Best Local Similarity 71.1%;
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بارد. مرابع موج

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/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
10-NORMALIZED"
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                                                                                                                                                                                                                                                                                                                                                        Gaps
             http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODJ015BF10NP1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                          Length 929;
                                                                                                                                                                                                                                                                           48 others
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Pred. No. 6.8e+02;
5; Mismatches 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : fliang@lifetech.com
                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                        16.5%;
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Best Local Similarity 68.4%;
Matches 542; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 929)
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BP 191 91006 EVRY cedex - France
Bmall: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8901.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgl?seq-CSODJO15BF10NP1&cluster=8901.f. Contact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATTGCTTGAACCCGGGAGGCAGACGTTGCAGTGAGCCGACATCACACTTTGCACTCCAG
                            CCACCGCGCCCGGCCATGATCATCTTGACTATGCT----GATGTGACAAGTACCTAA
                                                                                                                                                                                                                                                                                                                                                        AGCCATCAGACTCTACCCTTTAAATATGCAGTTTGGGCCAGGCACCGTGGCTCATGCCTG
                                                                                                                                                                                                                                                                                                                                                                              AGTACAGTGGCATCAGTTCACTGCAACCTCTGCCTCCCAGGTTCAAGCGATTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTATTTTTTATTTTATTATTTTTTTTTTTTTTGAGACCTAGCCTAGCTTGTCACCCAG
                                                                                                                                                          AATTTTTTTTTTTTTTTTTTGTAGAGGGGGTTTCACCGTTTTAGCCGGGATGGCCTCGAT
                                                                                                                                                                                                                        CTCCTGACCTCGTGATCCGCCCGCCTCGGCTCCCAAAGTGCTGGGATTACAGGCGTGAG
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                                                                                            gi:12946748
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Li,W.B., Gruber,C.
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/organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="Laxon:9606"
/clone="INAGE:3833367"
/tissue_type="adenocarcinoma cell line"
/lab_host="DHLOB (phage-resistant)"
/clone_lib="NIH_MGC_9"
/cl
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 701)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
High quality sequence stop: 666.
                                                                                 301 TGCCTGGCCTTTTATTTTGTGTGTGTGTTTTGATTTCTGACTTGGCCTTTTTAAAAAAATC
                                                                                                                                                                     412 ACTTTGGGAAGCCGAGGTGGGCAGATCAC--GAGATCAGGAGATCGAGACCATCCTGGCT
                                                                                                                                      709 CICTACCCTITAAAIATGCAGTTTGGGCCAGGCACCGTGGCTCATGCCTGTAATTCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCGTGGGGCACACCTGTAATCCCAGCTATGCTGGAGGCTGAGGCACGAGAGTCACTTGA
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.2%; Score 324; DB 10; Length 701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
Contact: Robert Strausberg, Ph.D.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ota'T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
352 ITTTTTTTTTTTTTTTTTTTTTTGAGACGGAGTCTCGCTC-TGTCGCCCAGGCTGGAGT
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/dev_stage="embryo, 10 weeks"
/clone_lib="HEMBB1"
/note="Vector: pME18SFL3"
161 c 163 g 167 t f othware
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
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Pred. No. 1e+03;
0; Mismatches 148;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEMBB1000637"
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AU120416.1 GI:10935651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human cDNA project
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Contact: Takao Isogai
Genomics Laboratory
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al Similarity 74.7%;
489; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2772)
Strausberg, R.
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Submitted (15-COT-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                              AGTTTGGGCCACGCACCGTGGCTCATGCCTGTAATTCCAGCACTTTGGGAGGCAGAGGTG
                                                                             GCTGGAGTGCAGTGGCGGGATCTCGGCTCACTGCAAGCTCCGGCCTCCCGGGTTCACGCCA
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                                  TCTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGAGGGAGTCTCGCTCTGTCGCCCAG
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              Gaps
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Email: cgapbs r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) &
Toshiyuki and Piero Carninci (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTC Homo sapiens, Similar to hypothetical protein FLJ20489, INAGE:5263792, mRNA.
BC038630
BC038630.1 GI:24116283
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            48;
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Pred. No. 1e+03;
); Mismatches 125; Indels
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 73.48;
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                                                                                                                                                     through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 73 Row: i Column: 4
This clone has the following problem: retained intron.
Location/Qualifiers
                                                                                Anuradha
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurad
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2772;
                                                                                                                                       Clone distribution: MGC clone distribution information
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                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5263792"
/tissue_type="Brain, hippocampus"
/clone_lib="NIH_MGC_95"
/lab_host="DHI08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 321.6; DB 11;
Pred. No. 3.9e+02;
0; Mismatches 174;
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ilarity 72.4%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 709)
E Hattori,M., Ishli,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q
E Q bases 1 to 709)
E J (bases 1 t
                                                           1889 AGCTGGGAGCAAATCCCCCCACCCCTACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGG 1948
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Homo sapiens genomic DNA, 21q region, clone: f2G2X4, genomic survey
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201 GCCCAGAGCCCAGGAGGAGGCAGTGGCCAGGAAGTGCAGGCCTGAGAAATCCGCGGCTG 142
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0; Mismatches 139; Indels
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="21"
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/clone="f2G2X4"
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Cercopithecus aethiops

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Butheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Cercopithecus.

(bases 1 to 381)

Minhas,R., Zhang,X., Dore,C., Villeneuve,A., Lepage,P., Forgetta,V.,

MCKee,K., Ophoff.R.A., Fairbanks,L.A., Freimer,N.B., Ervin,F.R.,

Palmour,R.M., Hudson,T.J. and Dewar, K.

UCLA/MUGQ/St-Kitts Vervet Monkey Mapping Project
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//cell_type="white blood cell"
//cell_type="white blood cell"
//clone_lib="CHORI-252 Vervet Monkey Library"
//clone_lib--252 Vervet Monkey Library
//c
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381 bp DNA linear GSS 28-APR-20
MUGQ_CH252P004Q3T7_M05_CD318_034 CHORI-252 Vervet Monkey Library
Cercopithecus aethiops genomic clone CH252-4B9, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               740 Dr. Penfield Room 7214, Montreal, QC, Canada, H3H 1A4
Tel: 514 398 3311 x00089
Fax: 514 398 1795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Dewar K
McGill University and Genome Quebec Innovation Centre
McGill University
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Class: BAC ends.
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/mol_type="genomic DNA"
/db_xref="taxon:9534"
/clone="CH252-4B9"
                                                                                                                                AAATAAATAAACAAACGAACAA 1053
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with an cligc-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pyTyT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The TAG_LIB=UI-H-DFO TAG_LIB=UI-H-DFO TAG_LIB=UI-H-DFO TAG_LIB=UI-H-DFO TAG_LIB=UI-H-DFO TAG_CIB=UI-H-DFO TAG_CIB-UI-H-DFO TAG_CIB

TAG_SEQ=GTTAAGCGTC"

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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.ed
The following repetitive elements were found in this cDNA
sequence: 11-300, >ALU (matched compliment) 366-655, >ALU 506-710,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA428305 710 bp mRNA linear EST 07-NOV-2002 UI-H-DF0-ber-e-18-0-UI.S1 NCI_CGAP_DF0 Homo sapiens cDNA clone UI-H-DF0-ber-e-18-0-UI 3', mRNA sequence.
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/lab_host="DHIOB (Life Technologies)"
/lab_host="DHIOB (Life Technologies)"
/clone_lib="NCI_CGAP_DFO"
/note="Organ: Bone; vector: pT/T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_DFO is a cDNA library containing the following tissue(s): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 710)

1 (CacAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished
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/db_xref="taxon:9606"
/clone="UT-H-DP0-ber-e-18-0-UI"
/tissue_type="Subchondral Bone"
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CA428305.1 GI:24791031
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Homo sapiens
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CA428305
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AUTHORS
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Best Local Similarity 72.0%;
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Human secreted/tra

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Scoring table:

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kallikrein-like protein; serine protease; cytostatic; cancer;
prostrate cancer; ds.
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                                                 AAZ65070
AAS21471
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ABK28605
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ACA04251
ABX89368
ABX80318
ABX80822
ABX81205
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Copyright (c) 1993 - 2003 Compugen Ltd.
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WPI; 2000-587440/55

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Score

Result No.

Human kallikrein e Human G-protein-co

G-protein-co breast cance BS247 specif BS247 specif cDNA differe neuroblastom IL-1ra BAC c phospholipas immune/haema IL-1ra BAC c prostate exp

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PG-3 gene. PG-3 gene SE

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EST-derived lung cancer

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The present sequence is the coding sequence of the human KLK-LZ gene, which encodes a kallikrein-like protein. Kallikreins and kallikrein-like proteins are a subgroup of the serine protease enzyme family. They catalyse the selective cleavage of specific polypeptide precursors to release peptides with potent biological activity. Nucleic acids encoding KIR-LI, KIK-LZ, KIK-LZ, KIK-LZ, KIK-LZ, KIK-LZ, KIK-LZ, MIK-LZ, MIK-LZ, MIK-LZ, MIK-LZ, and monitoring and diagnosis of cancers, especially prostrate cancer. They monitoring and diagnosis of cancers, especially prostrate cancer. They mediate the biological activity of the proteins. Antibodies can be used to identify a substance that can associate with or mediate the biological activity of the proteins. Antibodies can be used to treat conditions mediated by the kallikrein-like proteins.
                                                 (KLK-L) proteins for diagnosing and orders, especially cancer.
                                                                                                                                  Page 143-149; 184pp; English
                                                 New kallikrein-like (KLK-L)
protein mediated disorders,
P-PSDB; AAB21296
                                                                                                                                  Claim 1;
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Sequence 11570 BP; 3033 A; 2562 C; 3326 G; 2649 T; 0 other;

9980 TATTATAGGAGGTAATTATAGGGAGGTATGGGGAATTGAAGACAGGAAACACAAATTAG GGAGACATTTTTGGTTGTCACAACTATATGGAGGGGCATTACTGGCAACTAATGGATAGA **AAACAGACCAAAAACTTCCTGCCGCTGGACCTCATGTTCCCCAAGTGGAAGACAGGGCAA** CGTTTGAGGCTGCGGTAAGCCATGACTGCACTGCTGCACTCCAGACAGCAGCCTGGGTGA CGTTTGAGGCTGCGGTAAGCCATGACTGCACTGCTGCACTCCAGACAGCAGCCTGGGTGA GAGGAAGGAAGGAAAGGAAAAAAAAAAAAAAAAATGACTGTTGAAGAGCAGTGAGTAT TATTATAGGAGGGTAATTATAGGGAGGTATGGGGGAATTGAAGACAGGAAATTAG GGAGACATTTTTGGTTGTCACAACTATATGGAGGGGCATTACTGGCAACTAATGGATAGA TGCCAAGTGTGCTGTTCAACATGCTATGATGCACACGGCAGGCCTCCACAACAAACCATT DB 21; Length 11570; ö Indels 5, 99.6%; Score 2063; D 99.8%; Pred. No. 0; 11ve 0; Mismatches sal Similarity 99.8 2066; Conservative 9560 9620 9680 9740 0086 9860 9920 10100 -9500 61 121 181 241 301 361 421 481 601 Query Match 661 10160 Best Local Matches 206 õ g ŏ q g ò ď ò qq à g οy 셤 ð qq ò g à g ò g q ò

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       AAGAGGAAGATGGAGTGGAGAGTGACAAATGGGGTCTAAAGGTTGAACTTGGAGGCCAGG
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                               1921 CTCTCTAGTTGAACCTGGGAACAATTTCCAAAACTGTCCAGGGCGGGGGTTGCGTCTCA
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The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in activity and can be used in gene therapy. MI can be used for screening anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the structure and/or properties of the agent. MI can be used in the creatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adencer, or adencerinoma, carcinoma, clear cell cancer, infilitrating ductal cancer,
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Ebner R, Endress G,
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Carter KC,
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The present invention describes a method (MI) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 93% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening in the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the structure and/or properties of the agent. MI can be used in the structure and/or properties of the agent. MI can be used in the creatment of cancer such as colon, breast, stomach, lung, thyroid, cospobhageal, ovarian, kidney, prostate or pancreatic cancer, infiltrating ductal cancer.
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                                                                                                                                           2010 TCAGGGCCCATCCCTTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAACTGAGA 2069
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                                                                                                                                                                             141 CAAAACTGTCCAGGGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTCATCCTCAAGC
                              CAAAACTGTCCAGGGGGGGGTTGCGTCTCAATCTCCCTGGGGGCACTTTCATCCTCAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Breast cancer related gene sequence SEQ ID NO:2333.
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ID ABL63996 standard; DNA; 586 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptides. The sequences are useful for treating cancer, preferably breast cancer, in a patient or for stimulating an immune response. The polynucleotides and polypeptides are also useful in the diagnosis and monitoring of breast cancer. A method for detecting the presence of a cancer in a patient, comprises obtaining a biological sample from the patient, contacting the biological sample with a binding agent that bind to a breast tumour polypeptide, detecting in the sample an amount of polypeptide to a predetermined cut-off value, therefore determining the presence of a cancer in the patient. Sequences ABK29020-ABK29025 represence of a cancer in the patient. Sequences ABK29020-BEK29025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; breast tumour polypeptide; gene; ss; breast cancer; cytostatic;
  320 CCGCCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAGACCCTCATTCCTTC
                               1830 CCAGAGATGTTGAGAATGTTCATCTCTCCAGCCCCTGACCCCATGTCTCCTGGACTCAGG
                                             260 CCAGAGATGTTGAGAATGTTCATCTCTCAGCCCTGACCCCATGTCTCTCTGGGCTCAGG
                                                                                     1890 GTCTGCTTCCCCCACATTGGGCTGACCGTGTCTCTAGTTGAACCCTGGGAACAATTTC
                                                                                                      1950 CAAAACTGTCCAGGGCGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTCATCCTCAAGC
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ID ABK29013 standard; cDNA; 735
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12-OCT-2000; 2000US-0687507.
06-FEB-2001; 2001US-0778381.
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AG 19
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                22
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A novel isolated polypeptide comprising an immunogenic portion of a breast cancer protein useful in the detection and treatment of breast
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                                                                                                                                                                                                                                                         Human; breast tumour antigen; cytostatic; immunotherapy; breast cancer; vaccine; ss.
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                                                                                                                                                                                                                              cDNA sequence of human breast
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ID AAC79469 standard; cDNA; 735
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482; Conservative
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1650 GGAGATTACCCTTGTGCCCGGCCCAACAGACCGGGTGTCTACACGAACCTCTGCAAGTTC 1709
                                                                                             This sequence encodes a human breast tumour protein immunogenic fragment of the invention. The polypeptides or nucleic acids encoding them are useful in vaccines and pharmaceutical compositions for manufacture of medicaments for inhibiting the development of breast cancer in a patient. They can also be used to treat breast cancer. Antibodies against these polypeptides can be used to detect and monitor progression of breast polypeptides can be used to detect and monitor progression of breast encoding the breast proteins are useful for detection of breast cancer. Peripheral blood cells from a patient incubated in the presence of at least one polypeptide, such that T cells proliferate, are useful in manufacture of a medicament for treating breast cancer in a patient. Antigen presenting cells incubated in the presence of at least one polypeptide are also useful for treating breast cancer.
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                         'breast tumour protein genes used, in vaccines for immunotherapy, for diagnosis of breast cancer
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100.0%; Pred. No. 5.7e-81;
iive 0; Mismatches 0;
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                                                                       Claim 3; Page 70; 70pp; English.
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Matches 482; Conservative
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                                                                                                                                                                                                                             180 ACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCCTGAGTCATCCCAGGACTCAGACA
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                                                                                                          500 CAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCTGCAGGGACTCGTGTCTGG
                                                                                                                                                                    1770 CCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAGACCCTCATTCCTTC
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                            Length 735;
                                                            Indels
Sequence 735 BP; 161 A; 176 C; 226 G; 172 T; 0 other;
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                              Score 482; DB 24;
Pred. No. 5.7e-81;
                    development; therapy; ss
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97US-0998253.
97US-0998255.
98US-0118554.
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                                                             Conservative
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                              Query Match
Best Local Similarity
Matches 482; Conserv
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24-DEC-1997;
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                                1171 CAAAACTGTCCAGGGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTCATCCTCAAGC 1230
1950 CAAAACTGTCCAGGGGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTCATCCTCAAGC
                                                                      2010 TCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAACTGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                 BS247; detection; diagnosis; breast cancer; atypical hyperplasia;
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Hodges SC, Klass MR, Kratoch
Yu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                        fibroadenoma; cystic breast disease; gene therapy; ss.
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100.0%; Pred. No. 6.1e-81;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                       AAX57990 standard; DNA; 1302 BP.
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97US-0063431.
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, Stroupe SD,
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Russell JC,
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Matches 482;
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The invention relates to a method of detecting the presence of a target BS247 polynucleotide, especially mRNA, in a test sample. BS247 polynucleotides are derived from breast tissue. The polynucleotides, polynucleotides are useful for providing information leading polynucleotides are useful for providing information leading polynpeptides or antibodies are useful for providing information leading to the detection, diagnosis, staging, monitoring, prognosis, in vivo imaging, prevention or treatment, determining predisposition to, diseases and conditions of the breast, such as breast cancer, atypical hyperplasia, fibroadenoma and cystic breast disease. Drug treatment or gene therapy for breast cancer, can be based on these identified gene sequences and the efficacy of any particular therapy can be monitored. The BS247 derived reagents are advantageous for detection of breast cancer due to their specificity. The reagents also provide an alternative, non-surgical diagnostic method capable of detecting early stage breast disease, such as cancer.
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             BS247; detection; diagnosis; breast cancer; atypical hyperplasia; fibroadenoma; cystic breast disease; gene therapy; ss.
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Hodges SC, Klass MR, Kratochvil JD;
Yu H;
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Pred. No. 6.1e-81;
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100.0%; Pred. No. v...
0; Mismatches
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                                                                    Homo sapiens
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This sequence is a BS247 specific polynucleotide.

The invention relates to a method of detecting the presence of a target BS247 polynucleotide, especially mRNN, in a test sample. BS247 polynucleotides are derived from breast tissue. The polynucleotides or antibodies are useful for providing information leading to the detection, diagnosis, staging, monitoring, prognosis, in vivo imaging, prevention or treatment, determining predisposition to, diseases and conditions of the breast, such as breast cancer, atypical hyperplasia, fibroadenoma and cystic breast disease. Drug treatment or gene therapy for breast cancer, can be based on these identified gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer due to their specificity. The reagents also provide an alternative, non-surgical diagnostic method capable of detecting early
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Human secreted protein gene
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                               GGAGATTACCCTTGTGCCCGGCCCAACAGACCGGGTGTCTACACGAACCTCTGCAAGTTC
                                                            ACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCCTGAGTCATCCCAGGACTCAGCACA
                                                                      CCAGAGATGTTGAGAATGTTCATCTCCAGCCCCTGACCCCATGTCTCCTGGACTCAGG
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                    GGAGATTACCCTTGTGCCCGGCCCAACAGACCGGGTGTCTACACGAACCTCTGCAAGTTC
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Soppet DR;
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Ruben SM,
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Rosen CA,
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This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number is given in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human numunoglobulin Fer portion (e.g. AAZ06210) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 36 novel genes and their fragments (nucleic acid sequences: AAZ06219_206263; amino acid sequences AAY3848). Which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in polypectides. Specific uses are described for each of the 36 polynucleotides, based on which tissues they are most highly expressed in (see AAZ06219 for described uses).
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100.0%; Pred. No. 6.1e-81;
:Ive 0; Mismatches 0;
                                                     Claim 1; Page 173-174; 227pp; English.
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Best Local Similarity 100.
Matches 482; Conservative
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1150 CCAGAGATGTTGAGAATGTTCATCTCTCCAGCCCCTGACCCCATGTCTCTGGACTCAGG 1209
                                                                           1210 GICTGCTTCCCCCACATTGGGCTGACCGTGTCTCTTAGTTGAACCCTGGGAACAATTTC 1269
                                                                                                                                                                                        This DNA encodes a human keratinocyte derived protease (KDP) polypeptide. The protease is substantially similar to a sequence encoded by the insert in plasmid FERM BP-6129. The KDP polypeptide, from human keratinocytes, is specifically used in skin care products, particularly to treat or prevent skin flaking, e.g. dandruff, and in laundry detergent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Keratinocyte derived protease; KDP; protease; keratinocyte; human;
skin care product; skin flaking; dandruff; laundry detergent composition;
cleaning composition; dishwashing product; ss.
                                                                                                                            1270 CAAAACTGTCCAGGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTCATCCTCAAGC
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           Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obseity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroidtis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotides, based on which tissues they are most highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               secreted human protein. The gene number is given in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. ARZ06210) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 36 novel genes and their fragments (nucleic acid sequences: ARZ06219-Z06263; amino acid sequences ARX78386*738498) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 36
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Pred. No. 6.2e-81;
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100.0%; Pred. No. ...
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Ruben SM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognilive disorder; schizophrenia; prostate; obseivy; osteoclast; thymus; osteoporosis; arthitis; testis; lung; thyroid; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                            1134 ACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCTGAGTCATCCAGGACTCAGCACA
                                                                                                                            1314 GTCTGCTTCCCCCACATTGGGCTGACCGTGTCTCTTAGTTGAACCCTGGGAACAATTTC
                                                                                                                                                                                                                                                                                                                            CAAAACTGTCCAGGGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTCATCCTCAAGC
                                                                                                                                                                                                                                                                                                                                        1590 CAGGGTGATTCTGGGGGCCTGTGGTCTGCAATGGCTCCCTGCAGGGACTCGTGTCCTGG
                                                                                                          1014 CAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCCTGCAGGGACTCGTGTCCTGG
                                                                                                                                                                                                                                                                                       GTCTGCTTCCCCCACATTGGGCTGACCGTGTCTCTCTAGTTGAACCCTGGGAACAATTTC
                                                                                                                                                                   ACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCCTGAGTCATCCCAGGACTCAGCACA
                                                                                                                                                                                                         CCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAGACCCTCATTCCTTC
                                                                     Gaps
 can be used in
          products
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                                                 Length 1499;
                                                                    Indels
 compositions. More generally the KDP polypeptide can be
cleaning composition, e.g. hard surface or dishwashing
                            322 T; 0 other;
                                                           6.2e-81;
                                                                     ö
                                               DB 20;
                                              Match 23.3%; Score 482; DB Local Similarity 100.0%; Pred. No. 6.2 les 482; Conservative 0; Mismatches
                            Sequence 1499 BP; 310 A; 469 C; 398 G;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number is given in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene stability of the fused protein as compared to the human numunoglobulin Fc portion (e.g. AAZ06210) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 36 novel genes and their fragments (nucleic acid sequences: AAZ06219-Z06263; amino acid sequences AAY38386-Y38498) which are useful for preventing, treating or ameliorating medical conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polypucleotides. Specific uses are described for each of the 36 polynucleotides, based on which tissues they are most highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1590 CAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCCTGCAGGGACTCGTGTCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAGATTACCCTTGTGCCCGGCCCAACAGACCGGGTGTCTACACGGAACCTCTGCAAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAGATTACCCTTGTGCCCGGCCCAACAGACCGGGTGTCTACACGAACCTCTGCAAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCCTGAGTCATCCCAGGACTCAGCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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100.0%; Pred. No. 6.2e-81;
ive 0; Mismatches 0;
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                                                                                                                                                                                Lafleur |
Soppet |
                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 163-164; 227pp; English.
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98US-0070704.
98US-0070657.
98US-0070658.
98US-0070692.
                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
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Matches 482; Conservative
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                                                                                                                   Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand; pharmaceutical; receptor immunoadhesin; gene mapping; ss.
                                                                                            Membrane-bound protein PRO1132 encoding cDNA.
                        AAZ65070 standard; cDNA; 1570 BP
                                                                                                                                                                                                                                                98US-0087607
98US-00877609
98US-00877827
98US-0088021
98US-0088021
98US-0088028
98US-0088029
98US-0088031
98US-008881
98US-008891
98US-00891
98US-0089538
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98US-0089538
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                                                                      (first entry)
                                                                                                                                                       Homo sapiens
                                                                                                                                                                             409963088-A2
                                                                      05-APR-2000
                                                                                                                                                                                                                           02-JUN-1999;
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                                               AAZ65070;
RESULT 13
AAZ65070
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1437 CAAAACTGTCCAGGGGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTCATCCTCAAGC 1496
                                TCAGGGCCCATCCCTTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAAACTGAGA 2069
                                               Human secretory and transmembrane; PRO; mammalian; cancer; lung;
breast; prostate; cervical; tumour necrosis factor alpha; TMF-alpha;
cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
adipocyte; A-peptide; factor VIIA; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gao W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bloactive molecules to cells expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deforge L, Desnoyers L, Filvaroff E, A, Godowski PJ, Gurney AL, Sherwood S Tumas D, Watanabe CK, Wood WI, Zhang
                                                                                                                                                                                                                                                                                                     Human cDNA sequence encoding for PRO1132 polypeptide.
                                                                                                                                                                                                           AAS21471 standard; cDNA; 1570 BP.
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99US-0170262
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99WO-US28551
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                                                                                                                                                                                                                                                                         (first entry)
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Smith V, Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-408281/43.
P-PSDB; AAU12399.
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| AG 1558
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22-FEB-2000;
24-FEB-2000;
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02-JUN-2000;
10-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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20-MAR-2000;
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30-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1590 CAGGGTGATTCTGGGGGGCCTGTGGTGCTAATGGCTCCCTGCAGGGACTCGTGTCCTGG 1649
                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially
                                                                                                                                                                                                                                                                                                                                                                                                                  The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1077 CAGGGTGATTCTGGGGGGCCTGTGGTCTCCCATGCTCCCTGCAGGACTCCTGTGTCCTGG
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                                                                                                                                                                                                                                                                                                                                                         Membrane-bound proteins and related nucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1570 BP; 332 A; 485 C; 424 G; 329 T; 0 other;
                                                                                                                                                                                                                                                            Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 482; DB 21;
Pred. No. 6.2e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.3%; Sco. 100.0%; Pred. No. ... 0; Mismatches
                                                                                                                                                                                                                                                            Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Fig 225; 822pp; English.
                                                                                                                                                                                                                                                            Goddard A,
                                                                                 980S-0097974
980S-0097978.
980S-0097979.
980S-0097986.
                                                       98US-0097955
                                                                                                                                                                  98US-0098525
                                                                                                                                                                                98US-0100634
99US-0115565
                                                                        98US-0097971
                                        98US-0097954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by recombinant techniques.
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                                                                                                                                                                                                                                (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                          WPI; 2000-072883/06.
P-PSDB; AAY66726.
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                                                                                                                                                                                                                                                            Chen J,
Yuan J;
                                                                                                                                                                  31-AUG-1998;
                                                                                                                                                                                               12-JAN-1999
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Matches 482;
                                                                                     26-AUG-1998
26-AUG-1998
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(first entry)

02-APR-2001

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ARS21244-AAS21518 encode for novel human secretory and transmembrane PRO polypeptides are useful to detect other PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to Indulate biological activities of cells expressing PRO polypeptides, to modulate biological activities of cells expressing pRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation of chondrocytes, the proliferation of inner ear utricular supporting cells or cartilage, the release of a cytokine from peripheral blood monocytes (PBMCS), or the proliferation of endothalial cells. Some of the PBO control of the PRO control of Endothalial cells.
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                                                                                                                                                                                                                                                                                                                                                                          the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding
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  presence of mammalian tumours e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRO polypeptides can be used to generate probes, antisense RNA/I
transgenic or knock out animals and can be used in gene therapy.
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482; Conservative 0; Mismatches
and detect the
                                                            813pp; English.
                      lung, breast, prostate, cervical
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  polypeptides,
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                                                            Claim 3;
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AAF44216 standard; cDNA; 1570 BP.

RESULT 15 AAF44216

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The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of biocactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44470 to AAF44470 represent PCR primers and hybridistation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein
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Godowski PJ;
Paoni NF;
Wood WI;
                                                                                     Human; secreted and transmembrane protein; PRO; cytostatic; cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death -
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Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A,
Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J,
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
                                                          Human PRO1132 (UNQ570) nucleotide sequence SEQ ID NO:308.
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diagnostic assay; ss.
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Zhang Z;
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                                                                                             Gaps
sequences given in the exemplification of the present invention
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                                                         Query Match 23.3%; Score 482; DB 22; Length 1570; Best Local Similarity 100.0%; Pred. No. 6.2e-81; Matches 482; Conservative 0; Mismatches 0; Indels 0
                               Sequence 1570 BP; 332 A; 485 C; 424 G; 329 T; 0 other;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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|---------------|------------|-------|----------------|--------|----|-------------------|-------------------|
| Result No. | ult No. | Score | Query Match | Length | DB | ID | Description |
| ¦ 0 | : - | 482 | 23.3 | 735 | 4 | US-09-602-877A-94 | Sequence 94, Appl |
| | 7 | 482 | 23.3 | 1570 | 4 | -09-996-243- | |
| | ო | 476 | 23.0 | 1476 | ~ | US-08-824-874-2 | 7 |
| | 4 | 476 | 23.0 | 1476 | ٣ | US-09-210-084-2 | 7 |
| | Ŋ | 476 | 23.0 | 1476 | 4 | US-09-764-762-2 | 7 |
| | 9 | 460 | 22.2 | 1504 | 4 | US-09-280-116-1 | Sequence 1, Appli |
| | 7 | 222.6 | 10.7 | 176373 | ٣ | US-09-128-155-17 | 17, |
| O | œ | 219.4 | 10.6 | 70000 | 4 | US-09-851-896-3 | 3, |
| | 6 | 219.2 | 10.6 | 152331 | ო | US-09-128-155-16 | 16, |
| | 10 | 218.6 | 10.6 | 25464 | 4 | US-09-326-480A-4 | 4, |
| O | 11 | 216.4 | 10.4 | 461 | 4 | US-09-404-879A-1 | H |
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| | 17 | 215.6 | 10.4 | 3460 | 4 | US-09-904-615-44 | 44 |
| | 18 | 214.6 | 10.4 | 1001 | 7 | US-09-671-317-170 | 170, |
| | 19 | 214.6 | 10.4 | 1001 | 4 | US-09-671-317-450 | 450, |
| ပ | 20 | 4 | 10.4 | 41684 | 4 | US-09-536-059-1 | 1, Ar |
| ပ | 21 | 212.6 | 10.3 | 4421 | ~ | US-08-257-963B-9 | 6 |
| O | 22 | 212.6 | 10.3 | 4421 | 4 | US-08-367-841A-9 | 6 |
| ပ | 23 | 212.6 | 10.3 | 4421 | 4 | US-08-520-373D-6 | 9 |
| ပ | 24 | 212.6 | 10.3 | 4421 | ស | PCT-US95-07201-9 | 6 |
| O | 25 | 212.6 | 10.3 | 148567 | 4 | -09-801-876 | 3, |
| O | 26 | 212.2 | 10.2 | 99500 | 7 | US-09-798-096-10 | 10, |
| Ö | 27 | 210.4 | 10.2 | 38653 | 4 | US-09-922-445-1 | 1, 7 |

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| Sequence 3, Appli Sequence 33, Appli Sequence 33, Appli Sequence 33, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 10, Appli Sequence 1, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 1, Appli | THE THERAPY SR | Length 735; Indels 0; Gaps 0; CTGCAGGGACTCGTGTCTGG 1649 |
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| US-09-813-133A-3 US-09-740-041-3 US-09-88-88-497-33 US-09-362-230-33 US-09-78-894A-3 US-09-78-894A-3 US-09-64-469-3 US-09-671-317-485 US-09-671-317-485 US-09-671-317-485 US-09-671-317-485 US-09-671-317-485 US-09-671-317-485 US-09-671-317-485 US-09-671-317-485 US-09-671-317-485 US-09-671-317-485 US-09-671-800C-8 US-09-370-265-8 US-09-370-265-8 US-09-508-520-3730-4 US-09-608-285A-42 US-09-608-285A-42 | IGNMENTS A ND METHODS FOR O2,877A ion 3.0 | Score 482; DB 4; 0; Pred. No. 6.7e-92; 0; Mismatches 0; 0; CTGTGGTCTGCAATGGCTCC CCGCCTGCTTGCTTGCTTGCTCC CCGCCACAGCCGGTGTC CIIIIIIIIIIIIIIIIIIIIIIIIIIIII |
| 10.1 55827 4 10.1 66804 4 10.1 15328 4 10.1 15328 5 10.1 36651 4 10.1 49312 4 10.0 319608 4 10.0 9365 4 10.0 9365 4 10.0 9365 1 10.0 14747 4 | icati 7 7 7 0N: 7 Jiang 0N: 0N: 0N: NOS: EQ fc EQ fc | 23.38; mllarity 100.09 Conservative AGGGTGATTGGGGGG GAGTGATTACCTTGGGGGGGGGG |
| 209.2 209.2 209.2 209.2 209.2 209.2 209.2 200.2 207.2 2 207.2 2 207.2 2 207.2 | RESULT 1 US-09-602-877A-94/C Sequence 94, Applicat Patent No. 6432707 GENERAL INFORMATION: APPLICANT: Xu, Jian APPLICANT: Xu, Jian APPLICANT: Xu, Jian TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: 210 CURRENT APPLICATION CURRENT APPLICATION CURRENT APPLICATION CURRENT APPLICATION CURRENT APPLICATION CURRENT FILING DATE: NUMBER OF SEQ ID NOS SOFTWARE: FASTSEO F SEQ ID NO 94 LENGTH: 735 TYPE: DNA ORGANISM: HOMO SADI | Match Local S Local S 1590 1590 1650 1650 1650 1710 1710 1770 1770 1770 |
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R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088025
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APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/088029
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APPLICATION NUMBER: 60/088876
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FILING DATE: 1998-06-19
                          APPLICATION NUMBER: 60/088021
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APPLICATION NUMBER: 60/088861
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 2730P1C13

CURRENT APPLICATION NUMBER: 05/049787

PRIOR APPLICATION NUMBER: 60/06250

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-10-17

PRIOR PLICATION NUMBER: 60/065186

PRIOR PLICATION NUMBER: 60/065186

PRIOR PLICATION NUMBER: 60/06531

PRIOR PLICATION NUMBER: 60/06570

PRIOR PLICATION NUMBER: 60/075945

PRIOR PLILING DATE: 1997-11-24

PRIOR PLILING DATE: 1998-02-25

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PRIOR PLILING DATE: 1998-06-02

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PRIOR PLILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087609

PRIOR PLILING DATE: 1998-06-02

PRIOR PLILING DATE: 1998-06-02
140 CAAAACTGTCCAGGGGGGGGTGCGTCTCAATCTCCCTGGGGCACTTTCATCCTCAAGC 81
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US-09-996-243-308
Squence 308, Application US/09996243
Patent No. 6478825
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APPLICATION NUMBER: 60/087827
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy
Tumas, Daniel
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Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
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Eaton, Dan L.
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                                                                                                                                                                                                                                        1770 CCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAGACCCTCATTCCTTC 1829
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  1590 CAGGGTGATTCTGGGGGCCCTGTGGTCTGCAATGGCTCCCTGCAGGGACTCGTGTCCTGG 1649
                                 1077 CAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCCTGCAGGGACTCGTGGTCGTG
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CURPUIEN.
CURPUIEN.
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: Filed Herewith
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SPECIAL ON SPECIALOR:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
TILLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF-0252 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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| AG 1558
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US-08-824-874-2
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R APPLICATION NUMBER: 60/090676

R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090678

R FILING DATE: 1998-06-25

R FILING DATE: 1998-06-25

R FILING DATE: 1998-06-25

R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090694

R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090695

R APPLICATION NUMBER: 60/090695

R FILING DATE: 1998-06-25
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R FILING DATE: 1998-07-01

R APPLICATION NUMBER: 60/091478

R APPLICATION NUMBER: 60/091544

R APPLICATION NUMBER: 60/091544

R APPLICATION NUMBER: 60/091519

R FILING DATE: 1998-07-02

R APPLICATION NUMBER: 60/091625

R FILING DATE: 1998-07-02

R APPLICATION NUMBER: 60/091635

R FILING DATE: 1998-07-02

R APPLICATION NUMBER: 60/091635

R FILING DATE: 1998-07-02

R APPLICATION NUMBER: 60/091636

R FILING DATE: 1998-07-02
                                                                                                                         R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090252
R FILING DATE: 1998-06-22
R PILING DATE: 1998-06-22
R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090349
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FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/090863
FILING DATE: 1998-06-26
                           FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089952
FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/090246
                                                                                                                                                                                                                                                                                 FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090355
FILING DATE: 1998-06-23
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APPLICATION NUMBER: 60/090431
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090435
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090445
FILING DATE: 1998-06-24
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FILLING DAFE: 1998-06-24
APPLICATION NUMBER: 60/090535
FILLING DATE: 1998-06-24
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-24
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FILING DATE: 1998-07-07
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FILING DATE: 1998-07-09
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                        998-06-19
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Best Local Similarity 100.
Matches 482; Conservative
PRAILORR RELIGIOR PRAILORR RELIGIOR PRAILORR RELIGIORRE PRAILORRA RELIGIORRA RELIGIORRA
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1001 CAGGGTGATTCTGGGGGGCCTGTGCTCTGCAATGGCTCCCTGCAGGGACTCGTGTCCTGG 1060
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100.0%; Pred. No. 1.4e-90;
ive 0; Mismatches 0;
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STREET: 3174 Porter Drive
CITY: Palo Alto
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TITLE OF INVENTION: NOVEL KALLIKREIN
UMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: US/08/824,874
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Patent No. 6472195
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                                   ATTORNEY/AGENT INFORMATION:
NAME: B1111049, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                     LENGTH: 1476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 476; Conservative
                                                                                                                                                            TELEFAX: 415-845,4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COUNTRY: USA
ZIP: 94304
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CLONE: 820694
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US-09-764-762-2
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Best Local Similarity 100.0%; Pred. No. 1.4e-90;
Matches 476; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FSSLSED for Windows Version 2.0
SURTENY APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: Incyte Pharmaceuticals, Inc 3174 Porter Drive
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09210084 Patent No. 6197511
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IBM Compatible
                      LENGTH: 1476 base pairs
  SEQUENCE CHARACTERISTICS
                                       TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM MEDIUM TYPE: Diskett
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                                                                                                                       KERANOT02
                                                                               linear
                                                          STRANDEL.
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KERANO
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CITY: Palo Alto
STATE: CA
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                                                                                                                                                            US-08-824-874-2
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US-09-210-084-2
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1590 CAGGGTGATTCTGGGGGCCCTGTGGTCTGCAATGGCTCCCTGCAGGGACTCGTGTCT-G
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                        Encoding Human Protease
                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                        Length 1504;
                                                                                                                                                                                                                                                                                                                    Score 460; DB 4; 1
Pred. No. 3.1e-87;
0; Mismatches 0;
                                                                                                                                                                                                                                                          ; OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1997-08-04
SAUMBER OF SEQ ID NOS: 18
SOFTWARE: FASTSEQ for Windows Version 3.0
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules IFILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DAFE: 1999-03-26
SUMUMBER OF SEQ ID NOS: 268
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/09128155 Patent No. 6117654
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99.6%;
                                                                                                                                                                                                                                                                                                                        Query Match 22.2
Best Local Similarity 99.6
Matches 482; Conservative
                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
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                                                                                                                                                  SEQ ID NO 1
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                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 23.0%; Score 476; DB 4;. Best Local Similarity 100.0%; Pred. No. 1.4e-90; Matches 476; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PF-0252 US TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,762
FILING DATE: 16-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                   PRIOR AFFLICATION NUMBER: 09/210,084
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-09-280-116-1
Sequence 1, Application US/09280116A
; Patent No. 631427
; GENERAL INFORMATION:
                                            COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1476 base pairs
                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                        Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY: KERANOT02
CLONE: 820694
                                                                                                                                                                                        PRIOR APPLICATION DATA:
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPOLOGY: linear
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                                                          GAGGCTGAGGCAGGAGAATTGCTTGAACCCGGGAGATGGAGGCTGCAGTGAGCTGAGGTC 1312
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                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: AND USES THEREOF
TITLE REFERENCE: 094.04.022001
CURRENT APPLICATION NUMBER: US 60/091,650
EARLIER PILING DATE: 1998-08-03
EARLIER PILING DATE: 1998-08-03
EARLIER PELICATION NUMBER: US 60/091,650
EARLIER PILING DATE: 1998-08-03
EARLIER PILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SEQ ID NOS: 18
SEQ ID NOS: 18
SEQ ID NOS: 18
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Pred. No. 1.4e-36;
0; Mismatches 58;
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                                                                                                                                                                                                                                                                                   ; Sequence 16, Application US/09128155; Patent No. 6117654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16
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Best Local Similarity 81.4%;
Matches 254; Conservative
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US-09-326-480A-4
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APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEPEND FILE REFERENCE: FIS-0220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36312 TCACCTGAGGTTAGGAGTTCGAGACCAACCTGGCCAACATGGTGAAACCCCGTCTCTACT 36253
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                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                    Length 176373;
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Pred. No. 1.1e-36;
0; Mismatches 41;
                                                                                                                                                                                                    Score 222.6; DB 3;
Pred. No. 2.9e-37;
0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/851,896
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-851-896-3/c; Sequence 3, Application US/09851896; Patent No. 6410325
                                                                                                                    ; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C or
US-09-128-155-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127312 CCAAAAAAAAA 127324
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85.9%;
                                                                                                                                                                                                    Query Match
Best Local Similarity 84.0%;
Matches 263; Conservative
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Best Local Similarity 85.9
Matches 255; Conservative
                                                                                           NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
                  LENGTH: 176373
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 70000
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US-09-851-896-3
    SEQ ID NO 17
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1368 AA 1369
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Best Local Simi
Matches 255;
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                     APPLICANT: Henri-Jean Garchon
APPLICANT: Jean-Francois Bach
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE WHICH ENCODES A
TITLE OF INVENTION: RIAVIN MONOXYGENASE, THE CORRESPONDING PROTEIN AND THEIR
FILE REFERENCE: GENSET 064C1
CURRENT APPLICATION NUMBER: US/09/326,480A
CURRENT FILING DATE: 1999-06-04
PRIOR FILING DATE: 1997-12-05
PRIOR FILING DATE: 1997-12-06
PRIOR FILING DATE: 1996-12-06
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APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: LAGOZ
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 1.3e-36;
0; Mismatches 44
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 25464
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; Sequence 1, Application US/09404879A
; Patent No. 6468546
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85.0%;
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APPLICANT: Marta Blumenfeld
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ORGANISM: Homo sapiens
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER FILE REPERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
UNMBER OF SEQ ID NOS: 393
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                  .5e-36
                  Pred. No. 1.5e
0; Mismatches
 Score 216.4;
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              Best Local Similarity
Matches 255; Conserv
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
TITLE OF INVENTION: OF OVARIAN CANCER
FILE REPERENCE: 210121.463
CURRENT APPLICATION NUMBER: US/09/215,681A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 1.5e-36;
0; Mismatches 46
                                                   Score 216.4; DB 4
Pred. No. 1.5e-36;
0; Mismatches 46
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Best Local Similarity 84.4%;
Matches 255; Conservative
                                                   Query Match 10.4%;
Best Local Similarity 84.4%;
Matches 255; Conservative
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ORGANISM: Homo sapien
; ORGANISM: Homo sapien US-09-338-933-3
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US-09-215-681-1/c
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Patent No. 6488931
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT APPLICATION NUMBER: US/09/338,933
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APPLICANT: King, Gardon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
TITLE OF INVENTION: OVARIAN CANCER
FILE REFRENCE: 210121.46521
CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSEQ for Windows Version 3.0
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
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Search completed: August 5, 2003, 12:11:07 Job time : 136.302 secs

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BT006867 Homo sapi
BT007831 Synthetic
AY279380 Homo sapi
BD107879 36 human
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-Q=-Cq012_1/102FO_spool/TUG9936271/runat_04082003_104245_25702/app_query.fasta_1.455
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-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cd1 -LIST=45
-DOCALIGN=200 -THR_SCORE=FCT -THR_MAX=100 -ALIR_MIN=0 -ALIGN=15 -MODE=LOCAL
-USER=US0936271_CGCN -1 - 1 - 2326_CTUGA - 2 - 2326_CTUGA - 1 - 2326_CTU
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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synthetic construct
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1 (bases 1 to 882)
Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
Cloning of human full-length CDSs in BD Creator(TM) System Donor
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Staline, N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Woreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Farmer,A.
Direct Submission

Direct Submission

Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
Circle, Palo Alto, CA 94303, USA

This CDS clone is a part of a collection of human full length
expression clones generated by BD Biosciences Clontech and the
Harvard Institute of Proteomics. Each CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
tag). The CDS has been directionally cloned using BD In-Fusion(TM)
cloning system between the Sall and Hindill sites of the pDNR-DUAL
vector. Additional sequences in the clone: 'ACC' after Sall site
and before 'Hid III site to maintain reading frame.
Clone distribution: http://bioinfo.clontech.com/orfclones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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DAYPRQIDDTMFCAGDKAGRNSCQGDSGGPVVCNGSLQGLVSWGDYPCARPNRPGVYT
                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 882)
Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., Roundinga,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., Phelan,M. and Farmer,A.
Cloning of human full-length CDSs in BD Creator(TM) System Donor
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                     Homo sapiens kallikrein 5 mRNA,
BI006867
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                                                                                                 BT006867.1 GI:30582572
FLI_CDNA.
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Homo sapiens
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AY279380
1370 bp mRNA linear PRI 26-MAY-2003
Homo sapiens kallikrein 5 splice variant 1 (KLK5) mRNA, complete
Cds; alternatively spliced.
AY279380
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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( Dases I to 1370)

Kurlender. L. Yousef,G.M., White,N.M.A., Robb,J.-D., Borgono,C.A. and Diamandis,E.P.
Direct Submission
Submitted (19-APR-2003) Pathology and Laboratory Medicine, Mount Sinai Hospital, 600 University Avenue, Toronto, Ontario MSG 1X5, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identification of splice variants for the human kallikrien gene
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                                                                                                                                                                   ProHisProGlyTyrSerHisProGlyHisSerAsnAspLeuMetLeuIleLysLeuAsn
                                                                                                                                                                                            CCCCACCCTGGCTACTCCCACCCTGGCCACCTCTAACGACCTCATGCTCAAACTGAAC
                                                                                                                                                                                                                                                                 ArgarglleArgProThrLysAspValArgProIleAsnValSerSerHisCysProSer
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Kurlender, L., Yousef, G.M., White, N.M.A., Robb, J.-D., and Diamandis, E.P.
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/organism="Homo sapiens
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/db xref="taxon:9606"
/chromosome="19"
/map="19q13.4"
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/gene="KLK5"
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AY279380
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/note="Mutations: 881:Stop->Leu"
/codon_start=1
/transl_table=11
/transl_table=11
/product="Homo sapiens kallikrein 5"
/product="Homo sapiens kallikrein 5"
/product=10.1d="AAAR36503.1"
/db_xref="GI: 30584503.1"
/db_xr
                                                                                                          Circle, Palo Alto, CA 94303, USA
This CDS clone is a part of a collection of human full length
expression clones generated by BD Blosciences Clontech and the
expression clones generated by BD Blosciences Clontech and the
farvard Institute of Proteomics. Each CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
tags). The CDS has been directionally cloned using BD In-Fusion(TM)
cloning system between the Sall and HindIII sites of the pDNR-DUAL
vector. Additional sequences in the clone: 'ACC' after Sall site
and before 'ATG' to provide Kozak consensus sequence; 'GG' after
clone distribution: http://bioinfo.clontech.com/orfclones.
Location/Qualifiers
Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Kounding, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M. and Farmer, A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
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                                                                                              Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="BD Creator(TM) CDS Library derived from MGC collection"
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/note="Vector: pDNR-Dual"
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Matches:
Conservative:
Mismatches:
Indels:
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/mol_type="mRNA"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                    PAT 18-SEP-2002
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Mammalia; Eutheria; Arimates; Catarrhini; Hominidae; Homo.

T (bases 1 to 1381)

Ruben, S.W., Soppet, D.R., Ebner, R., Lafleur, D.W., Ni, J.,

Brewer, L.A., Olsen, H.S., Duan, R.D. and Rosen, C.A.

Brewer, L. A., 50 os 08-JAN-2002;

HUMAN GENOME SCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC A61P37/00,C07K14/435,C07K16/18,C12N1/15,C12N1/21,C12N5/10,C12N15/00,C12N15/00,C12N15/00
CC 36 human secreted proteins
FH Key Location/Qualifiers
           TrpGlyAspTyrProCysAlaArgProAsnArgProGlyValTyrThrAsnLeuCysLys
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PN 17 2002500035-A/50
PD 08-JAN-2002
PF 06-JAN-1999 JP 2000527554
PR 07-JAN-1999 US 60/070657,07-JAN-1998 US 60/070658
PN 07-JAN-1998 US 60/070659,07-JAN-1998 US 60/07069
PN RUBEN, DANIEL R SOPPET, REINHARD EBNER, DAVID W LAFLEUR, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers

1. 1381
/organism='Homo sapiens (human)'.

7. organism='Homo sapiens"
/mol_type='genomic DNA"
/db_xref="taxon:9606"

3 4 425 c 353
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Conservative:
Mismatches:
Indels:
Gaps:
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NCCKFTKNIQETIQANS"
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                                                  //note="serine protease; hK5; alternatively spliced; similar to the product of GenBank Accession Number AF135028"
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Mismatches:
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1319. 1324
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a 424 c
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E 2 (bases 1 to 1387)

Brattsand, M. and Egelrud, T.

Direct Submission

Dermatology and Venereology, Umea University, University Hospital,
Unea SE-901 85, Sweden

S Brattsand, M. and Egelrud, T.

Brattsand, M. and Egelrud, T.

Direct Submission

L Submission

L Submitted (16-APR-2002) Public Health and Clinical Medicine,
Dermatology and Venereology, Umea University, University Hospital,
Umea SE-901 85, Sweden

S Sequence update by submitter

S Sequence update by submitter

On Apr 16, 2002 this sequence version replaced gi:6063032.
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Brattsand,M. and Egelrud,T.
Purification, molecular cloning, and expression of a human stracorneum trypsin-like serine protease with possible function in
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Matches:
Conservative:
Mismatches:
Indels:
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involved in desquamation"
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/organism="Homo sapiens"
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                                                                     LeuGlyValThrGluHisValLeuAlaAsnAsnAspValSerCysAspHisProSerAsn
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1078 . 1138
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1887 . 1392
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Indels:
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GATGACAGCAGCAGCCGCATCATCAATGGATCCGACTGCGATATGCACACCCAGCCGTGG 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 1438)
Yousef,G.M., Robb,J.-D., White,N.M.A., Kurlender,L., Borgono,C.A.
and Diamandis,E.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (19-APR-2003) Pathology and Laboratory Medicine, Mount
Sinai Hospital, 600 University Avenue, Toronto, Ontario M5G 1X5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                identification of splice variants for the human kallikrien gene
(KhLK5)
                      TrpGlyAspTyrProCysAlaArgProAsnArgProGlyValTyrThrAsnLeuCysLys
                                                                                                                        TyrSerLeuSerProValTyrGluSerGlyGlnGlnMetPheGlnGlyValLysSerIle
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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C12N15/57,C12N9/64,A61K38/48,A61K7/48,C11D3/386,C07K16/40
                916 TGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCCTGCAGGGACTCGTGTCC
                                       AlaGlyThrLysCysLeuValSerGlyTrpGlyThrThrLysSerProGlnValHisPhe
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Kitado, H., Yoshikawa, A. and Zaiki, T.
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644" a 469 c 398 g 332
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Homo sapiens, kallikrein 5, clone MGC:1107 IMAGE:2989806, mRNA,
complete cds.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 6912643.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs remail.nih.gov
Tissue Procurement: DCTD/DTP
Tissue Procurement: DCTD/DTP
TOTAL Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The Total Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel DicKhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1536)
Strausberg, R.
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Submitted (21-MAZ-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                       AlaGlyThrLysCysLeuValSerGlyTrpGlyThrThrLysSerProGlnValHisPhe
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Contact: MGC help desk
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/mol_type="mRNA"
/db_xref="LocusID:25818"
/db_xref="taxon:9606"
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PN JP 2002500035-A/36
PD 08-JAN-2002
PP 06-JAN-1999 JP 2000527554
PR 07-JAN-1998 US 60/070657,07-JAN-1998 US 60/07065
07-JAN-1998 US 60/070692,07-JAN-1998 US 60/0707069
M RUBEN, DANIEL R SOPPET, REINHARD EBNER, DAVID W LAFLEUR, PI
           Ruben, S.M., Sopper, D.R., Ebner, R., Lafleur, D.W., Ni, J., Brewer, L.A., Olsen, H.S., Duan, R.D. and Rosen, C.A. 36 human secreted proteins Patent: JP 2002500035-A 36 08-JAN-2002; HUMAN GENOME SCIENCES INC S Homo saplens (human) PN JP 200250035-A/36 PD 08-JAN-2002
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/organism='Homo sapiens (human)'.
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                                                                        TrpG1yAspTyrProCysAlaArgProAsnArgProG1yVa1TyrThrAsnLeuCysLys
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Minterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.
Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.
Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.
Implant, method of making same and use of the implant for treatment of bone defects
treatment of bone defects
Patent: US 6478825-A 308 12 NOV-2002;
Location/Qualifiers
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Sequence 308 from patent US 6478825.
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DAYPRQIDDTMFCAGDKAGRDSCQGDSGGPVVCNGSLQGLVSWGDYPCARPNRPGVYT
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| Db 354 ATGGCTACAGCAAGACCCCCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTT 413 | Qy 21 LeuGlyValThrGluHisValLeualaAsnAsnAspValSerCysAspHisProSerAsn 40 | 0y 41 ThrValProSerGlySerAsnGlnAspLeuGlyAlaGlyAlaGlyGluAspAlaArgSer 60 | Qy 61 AspaspSerSerSerargileileasnGlySerAspCysAspMetHisThrGlnProTrp 80 | Qy 81 GlnalaalaLeuLeuArgProAsnGlnLeuTyrCysGlyAlaValLeuValHisPro 100 [111111111111111111111111111111111 | Qy 101 GlnTrpLeuLeuThrAlaAlaHisCysArgLysLysValPheArgValArgLeuGlyHis 120 (1111111111111111111111111111111111 | Qy 121 TyrSerLeuSerProValTyrGluSerGlyGlnGlnMetPheGlnGlyValLysSerIle 140 | Qy 141 ProHisProGlyTyrSerHisProGlyHisSerAsnAspLeuMetLeuIleLysLeuAsn 160 | Qy 161 ArgArg1leArgProThrLysAspValArgProIleAsnValSerSerHisCysProSer 180 | Qy 181 AlaGlyThrLysCysLeuValSerGlyTrpGlyThrThrLysSerProGlnValHisPhe 200 | Qy 201 ProLysValLeuGlnCysLeuAsnIleSerValLeuSerGlnLysArgCysGluAspAla 220 | 221 | Oy 241 CysGlnGlyAspSerGlyGlyProValValCysAsnGlySerLeuGlnGlyLeuValSer 260 | Qy 261 TrpGlyAspTyrProCysAlaArgProAsnArgProGlyValTyrThrAsnLeuCysLys 280 | Oy 281 PheThrLysTrp11eGlnGluThrIleGlnAlaAsnSer 293 | T 12 | AX403 ITION Seque SION AX403 ON AX403 RDS | SOURCE Homo sapiens (human) ORGANISM Homo sapiens DEMARYOLA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | REFERENCE 1 AUTHORS Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D., Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P., Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J., |
|---|---|---|---|--|--|--|--|---|---|---|----------|--|---|--|---|---|--|---|
| Db 714 TACTCCCTGTCACCAGTTTATGAATCTGGGCAGCAGGATGTTCCAGGGGGGTCAAATCCATC 773 | Qy 141 ProHisProGlyTyrSerHisProGlyHisSerAsnAspLeuMetLeullelySLeuAsn 160 | Qy 161 ArgArglleArgProThrLysAspValArgProIleAsnValSerSerHisCysProSer 180 | Qy 181 AladlyThrLySCysLeuValSerGlyTrpGlyThrThrLySSerProGlnValHisPhe 200 | Oy 201 ProLysValLeuGlnCysLeuAsnIleSerValLeuSerGlnLysArgCysGluAspAla 220 | <pre>Qy 221 TyrProArgGlnIleAspAspThrMetPheCysalaGlyAspLysAlaGlyArgAspSer 240 </pre> | <pre>Qy 241 CysGlnGlyAspSerGlyGlyProValValCysAsnGlySerLeuGlnGlyLeuValSer 260 </pre> | <pre>Qy 261 TrpGlyAspTyrProCysAlaArgProAsnArgProGlyValTyrThrAsnLeuCysLys 280</pre> | Qy 281 PheThrLysTrpIleGlnGluThrIleGlnalaAsnSer 293 | AX080829 | DEFINITION Sequence 75 irom Patent WOULU9327. ACCESSION AX080829 GI:13169796 KEYWORDS | <u>~</u> | CE 1 RS Ashkenazi,A.J., Baker,K.P., Goddard,A., Godowski,P.J., Gur Kljavin,I.J., Lafleur,M., Mark,M.R., Marsters,S.A., Pitti, Watanabe,C.K. and Wood,W.I | 1 | FEATURES LOCATION/QUALITIERS SOURCE 1. 1570 /Organism="Homo sapiens" /mol_type="genomic_DNA" | BASE COUNT 332 a 485 c 424 g 329 t ORIGIN | | | US-09-936-271B-14 (1-293) x AX080829 (1-1570) QY |

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PAT 16-JUL-2002
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Secreted and transmembrane polypeptides and nucleic acids encoding
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 Homo sapiens
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Sequence 455 from Patent WO0140466.
AX464322 AX464322.1 GI:21899177
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  Watanabe, C.K.,
Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Williams, P., Wood, W.I. and Zhang, Z. Secreted and transmembrane polypeptides and
                                                                                                                      Length:
Matches:
Conservative:
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Indels:
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                                    Genentech Inc. (US)
Location/Qualifiers
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/db_xref="taxon:9606"
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| 41 ThrValProSerGlySerAsnGlnAspLeuGlyAlaGlyAlaGlyGluAspAlaArgSer 60 | 577 120 637 140 697 | 160 nArgArglleArgProThrLysAspValArgProIleAsnValSerSerHisGysProSe | 200 eProLysValLeuGlnCysLeuAsnIleSerValLeuSerGlnLysArgCysGluAspAl 220 | 240 rCysGlnGlyAspSerGlyGlyProValValCysAsnGlySerLeuGlnGlyLeuValSe 260 | 280 sPherhrLysTrpIleGlnGlurhrIleGlnAlaAsnSer 293 | DEFINITION Sequence 2 from patent US 6197511. ACCESSION AR137506 ACCESSION AR137506.1 GI:14479015 ACCESSION AR137506.1 GI:1476 ACCESSION AR137506.1 GI:14479015 ACC | igin |
|---|--|--|--|--|---|--|--|
| rile 14 carc 77 caac 83 ccrc 89 | CCCCCAAGIGCACTIC 933 SAIGCYSGLUASPALA 220 [AAGGTGCGAGGATGCT 1013 SALAGIYALGASPSER 240 CACCAGGTAGAGACTCC 1073 DD | alser 260 | 0y Db ear PAT 31-AUG-2000 Db | 40 da | Oy Db RESULT RESULT | LD DE AC | CTAAC 396 |
| 121 TyrSerLeuSerProValTyrGluSerGlyGlnGlnMetPheGlnGlyValLysSerile | 894 GCTGGGACAAAGTGCTTGGTGTCTGGCGGGACAACCAAAAGCCCCCAAGTTC 201 ProbysValLeuGlnCysLeuAsn11eSerValLeuSerGlnLysArgCysGluAspAla | | | AR078184.1 GI:10004930 Unknown. Unclassified. I (bases 1 to 1476) Hillman,J.L. and Lal,P. | <pre>Human kallikrein Patent: US 5562300-A 2 05-0CT-1999; Location/Qualifiers 11476 /organism="unknown" 303 a 466 c 388 g 319 t</pre> | Scores: 1.57e-119 | 337 CTGGGGGTCACAGAGCATGTTCTCGCCAACAATGATGTTTCCTGTGACCACCCT |
| | 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 | 6y 24: Db 1107- Qy 26: Db 1133 Ov 28: | SULT 14 SOLT 14 COS CUS | ACCESSION VERWORDS SOURCE ORGANISM REFERENCE | J Č ₽ | Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similari Query Match: DB: US-09-936-271B-14 (CO) OY 1 MetAl | Dp 3 |

| Alignment Sc Pred. No.: Score: Percent Simi Best Local & Query Match: DB: | Scores: | 1.57e-119 1.555.00 99.66% 99.19% | Length: Matches: Conservative: Mismatches: Indels: Gaps: | 1476 293 0 0 1 | |
|---|----------------|---|--|--|------|
| us-09-936-2 | 2718-14 (1-29 | 3) x AR137506 | (1-1476) | | |
| oy d | 1 Metalathr | AlaArgProProTrp | MetTrpValLeuCysA | MetalaThralaArgProProTrpMetTrpValLeuCysAlaLeuIleThrAlaLeuLeu | 0 |
| | | GCAAGACCCCCTIGG | ATGTGGGTGCTCTGTG | F | 336 |
| | 21 LeuGl | ThrGluHisValLeu | yvalThrGluHisvalLeuAlaAsnAsnAspVal5 | SerCysAspHisProSerAsn | 40 |
| Dp 3 | 337 CTGGGGGTC | ACAGAGCATGTTCTC | GCCAACAATGATGTT | GACCACCCT | 396 |
| QY | 41 ThrValPro | SerGlySerAsnGln | AspLeuGlyAlaGlyA | ThrValProSerGlySerAsnGlnAspLeuGlyAlaGlyAlaGlyGluAspAlaArgSer | 09 |
| Dp 3 | 397 ACCGIGCCC | TCTGGGAGCAACCAG | GACCTGGGAGCTGGG | GICG | 456 |
| δy | 61 AspAspSerSe | rSerArgileil | eAsnGlySerAspCysAspMe | SpMetHisThrGlnProTrp | 80 |
| Db . 40 | 457 GATGACAGC | CAGCCGCATCAT | AATGGATCCGACTGC | SCACACCCAGCCGTG | 516 |
| Оу | 81 -GlnAlaAl | aLeuLeuLeuArgPr | -GInAlaAlaLeuLeuLeuLeuArgProAsnGlnLeuTyrCysGlyAlaValLeuVal | HisPr | 100 |
| qa | 517 GCAGGCCGC | GCTGTTGCTAAGGCC | CAACCAGCTCTACTGC | CATCC | 576 |
| 0y 1 | 100 oGlnTrpLe | uLeuThrAlaAlaHi | sCysArgLysLysVal | OGINTrpLeuLeuThrAlaAlaHiSCysArgLysLysValPheArgValArgLeuGlyHi | 120 |
| qq | 577 ACAGIGGCI | GCTCACGCCGCCCA | CTGCAGGAAGAAGTI | | 989 |
| 0y 1 | 120 sTyrSerLe | uSerProValTyrGl | uSerGlyGlnGlnMet | STyrSerLeuSerProValTyrGluSerGlyGlnGlnMetPheGlnGlyValLysSerIl | 140 |
| Op QQ | 637 CTACTCCCT | GTCACCAGTTTATGA | ATCTGGGCAGCAGATG | | 969 |
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| Dp qq | 697 cccccAccc | TGGCTACTCCCACC | TGGCCACTCTAACGAC | | 756 |
| 0у 1 | 160 nArgArgil | eArgProThrLysAs | pValArgProlleAsr | nArgArgIleArgProThrLysAspValArgProIleAsnValSerSerHisCysProSe | 180 |
| da 7 | 757 CAGAAGAAT | TCGTCCCACTAAAGA | TGTCAGACCCATCAAC | - r) | 816 |
| Oy 1 | 180 rAlaGlyTh | rLysCysLeuValSe | rGlyTrpGlyThrThr | rAlaGlyThrLysCysLeuValSerGlyTrpGlyThrThrLysSerProGlnValHisPh | 200 |
| Dp qa | 817 TGCTGGGAC | AAAGTGCTTGGTGTC | CGGCTGGGGGACAACC | | 876 |
| Oy 2 | 200 eProLysva | ProLysValLeuGlnCysLeuAs | SLeuAsnIleSerValLeuSer | 3lnLysArgCysGluAspAl | 220 |
| QQ . | 877 cccraaggr | CCTCCAGTGCTTGAA | TATCAGCGTGCTAAGT | CAGAAAAGGTGCGAGGATGC | 936 |
| Qy 2 | 220 aTyrProAr | OArgGlnIleAspAspThrMetPhe | CysAlaGly | AspLysAlaGlyArgAspSe | 240 |
| 6 qq | - 0 | ACAGATAGATGACAC | Tececce | GACAAAGCAGGTAGAGACTC | 966 |
| Oy 2 | 240 rCysGlnGl | yAspSerGlyGlyPr | oValValCysAsnGly | GlnGlyAspSerGlyGlyProValValCysAsnGlySerLeuGlnGlyLeuValSe | 260 |
| 6 qa | ည္က | TGATTCTGGGGGGCC | rerecrecaaree | | 1056 |
| 0у 2 | 260 rTrpGlyAs | pTyrProCysAlaAr | gProAsnArgProGly | GlyAspTyrProCysAlaArgProAsnArgProGlyValTyrThrAsnLeuCysLy | 280 |
| Db 10 | 057 CTGGGGAGA | TACCCTTGTGCCCG | GCCCAACAGACCGGGT | CAA | 1116 |
| Qy 2 | 280 sPheThrLy | STrpIleGlnGluTh | SPheThrLysTrpIleGlnGluThrIleGlnAlaAsnSer | . 293 | |
| Db 11 | 17 | GTGGATCCAGGAAAC | CATCCAGGCCAACTCC | 1156 | |

Search completed: August 5, 2003, 13:24:21 Job time : 3136 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. OM protein - nucleic search, using frame_plus_p2n model

(without alignments)
2886.625 Million cell updates/sec August 5, 2003, 05:55:25 ; Search time 274 Seconds Run on:

1608 1 MATARPPHMWVLCALITALL......VYTNLCKFTKWIQETIQANS 293 US-09-936-271B-14 Title: Perfect score: Sequence:

0.5 BLOSUM62 Xgapop 10.0, Xgapext (Ygapop 10.0, Ygapext (Fgapop 6.0, Fgapext (Delop 6.0, Fgapext Scoring table:

2552756 seqs, 1349719017 residues Searched: Total number of hits satisfying chosen parameters:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

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'gcgdata/geneseg/genesegn-embl/NA2002.DAT

and is derived by analysis of the total score distribution.

SUMMARIES

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| Res | Result No. | Score | Query Match L | Length | DB | ΩI | Description |
| 1 | п. | 1608 | 0. | 882 | 7 | 233 | PDSP-1 |
| | ~ | 1608 | 96 | 1302 | 200 | AAX57989 | Human BS247 specif |
| | ٥ ٨ | 1608 | 36 | 1381 | 2 0 | AAA37330 AA206259 | Human secreted ord |
| | . 7 | 1608 | 8 | 1499 | 20 | AAX60578 | Human keratinocyte |
| | 91 | 1608 | 00 | 1516 | 50 | AAZ06245 | Human secreted pro |
| | ~ 68 | 1608 | 100.0 | 1539 | 20 | AAZ65070 | Human PDSP-1 DNA. Membrane-bound pro |
| | 6 | 1608 | 8 | 1570 | 22 | AAS21471 | Human cDNA sequenc |
| | 10 | 1608 | 88 | 1570 | 22 | AAF44216 | Human PRO1132 (UNO |
| | 15 | 1608 | 38 | 1570 | 25 | AEN 28003 ACA 03830 | encoc |
| | 13 | 1608 | 100.0 | 1570 | 25 | ACA04251 | an cDNA en |
| | 4- 4 | 1608 | 96 | 1570 | 25 | ABX89368 | ncoding no |
| | 10 | 1608 | 88 | 1570 | 52 | ABX80822 | Human secreted of |
| | 17 | 1608 | 00 | 1570 | 25 | ABX81205 | |
| | 8 5 | 1608 | 000 | 1570 | 25 | ABX90295 | |
| | 5 5 | 1608 | 9 6 | 1570 | 2 C | ABX / / 906 | Human PRO polynuci |
| | 21 | 1608 | 100.0 | 1570 | 25 | ABX64141 | cDNA encoding huma |
| | 22 | 1608 | 00 | 1570 | 25 | ABX17105 | Human PRO polynucl |
| | 23 | 1595 | | 14/6 | 200 | AAX16295 AAX06260 | Human kallikrein e Human secreted pro |
| | 25 | 1403 | | 1504 | 24 | ABK30231 | |
| | 56 | 1002 | | 11570 | 21 | AAA95905 | KLK-L |
| C | 27 28 | 734 | | 455 | 20 | AAX57986 AAC79469 | Human BS247 specif |
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| ပ | 30 | 725 | | 738 | 20 | AAX84240 | coding |
| | 31 | 688 | | 673 | 22 | AAF44901 | Human breast cance |
| | 3 6 | 671 | 41.7 | 765 | 222 | AAS03914 AAH93821 | Human prostate-spe |
| | 34 | 671 | | 765 | 22 | AAH85135 | prostate-s |
| | 35 | 671 | | 765 | 24 | ABL95285 | P703P puta |
| | 3 C | 671 | | 765 | 2 2 | ACA39/22 AB083343 | Flostate cancer in Human KLK4 encodin |
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| | 39 | ິເຕ | ٠. | 1052 | 22 | AAF55270 | nbəs |
| | 40 | ഗ | 40.6 | 1146 | 20 | AAV84589 | secreted |
| | 4 7 | വ | 40.6 | 1146 | 22 | ABA83430 AAD14841 | Human secreted pro |
| | 7 7 | າທ | 40.5 | 833 | 61 | AAV42925 | coding a |
| | 44 | 650.5 | 40.5 | 1106 | 20 | AAZ22638 AAZ22639 | 312 nucleot 312 derived |
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| | | | | | | ALIGNMENTS | |
| RES AAZ ID | RESULT 1 AAZ23318 ID AAZ | 23318 | standard: | DNA: | 882 | | |
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| K K K | PD9 tre | PDSP-1; Ta treatment; | Tango 114; t; prolife | prost | ate- | derived serine protea | fusion p screening |
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| X X | sei | erine prot | ease; | human; | ds. | | |
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                             ProHisPrqGlyTyrSerHisProGlyHisSerAsnAspLeuMetLeuIleLysLeuAsn
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Hodges SC, Klass MR, Kratochvil JD;
Yu H;
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Gordon J, Granados EN,
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Russell JC,
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                                                                                                                                                                                                                                                                                                                           This invention describes a novel human prostate-derived serine protease (PDSP) polynucleotide (also known as Tango 114). The prostate derived serine protease (PDSP) polypeptide is used to modulate a variety of cellular processes. It can used to produce fusion proteins. PDSP is used to treat proliferative disorders, e.g. prostate cancer. The protein may also be used to produce antibodies, e.g. prostate cancer. The protein may can be used to produce antibodies, and to identify antagonists and antibodies can be used in Screening assays; predictive medicine; and methods of treatment. PDSP cleaves growth factors, and can be used for the modulation of growth factors blosynthesis; generation of active peptides, regulation of growth factor blosynthesis; generation of growth factor blosynthesis; generation; regulation of callular proliferation; development. The PDSP claudiation of proteins regulation of prostate development. The PDSP contestasis and regulation of prostate development. The PDSP collunctedides can be used to express the protein; to detect PDSP mRNA; to detect genetic alterations in the PDSP gene; in forensic biology; and solve protease and probes. As serine protease have important coles in cellular processes, there exists a need for identifying novel serine protease such as the prostate derived serine protease (PDSP) of the invention. This sequence encodes the human PDSP-1 described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
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                                                                                                                                                                                                                                                           . prostate derived serine protease polynucleotides and polypeptides to modulate cellular processes \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MetAlaThrAlaArgProProTrpMetTrpValLeuCysAlaLeuIleThrAlaLeuLeu
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Best Local Similarity:
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 Homo sapiens
                             WO9946391-A2
                                                                                         12-MAR-1999;
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This sequence is a BS247 specific polynucleotide.

The invention relates to a method of detecting the presence of a target
The invention relates to a method of detecting the presence of a target
SS247 polynucleotide, especially mRNA, in a test sample. BS247
polynucleotides are derived from breast tissue. The polynucleotides,
polynucleotides are useful for providing information leading
to the detection, diagnosis, staging, monitoring, presponsis, in vivo
imaging, prevention or treatment, determining predisposition to, diseases
and conditions of the breast, such as breast cancer, atypical
on therapy for breast cancer, can be based on these identified gene
sequences and the efficacy of any particular therapy can be monitored.
The BS247-derived reagents are advantageous for detection of breast
cancer due to their specificity. The reagents also provide an
alternative, non-surgical diagnostic method capable of detecting early
stage breast disease, such as cancer.
                                                                                                                                                                      201 ProLysValLeuGlnCysLeuAsnIleSerValLeuSerGlnLysArgCysGluAspAla
                                                                       TyrProArgGlnIleAspAspThrMetPheCysAlaGlyAspLysAlaGlyArgAspSer
                 Breast tissue derived cDNA contig and consensus polypeptide sequence
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Hodges SC, Klass MR, Kratochvil JD;
Yu H;
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                                                                                                                                                                                                                                            Human BS247 specific polynucleotide #8.
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28-OCT-1997;
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                                                                This sequence is a BS247 specific polynucleotide.

The invention relates to a method of detecting the presence of a target BS247 polynucleotide, especially mRNA, in a test sample. BS247 polynucleotides are derived from breast tissue. The polynucleotides, polynucleotides are derived from breast tissue. The polynucleotides, polynucleotides are useful for providing information leading to the detection, diagnosis, staging, monitoring, prognosis, in vivo imaging, prevention or treatment, determining predisposition to, diseases and conditions of the breast, such as breast cancer, atypical hyperplasia, fibroadenoma and cystic breast disease. Drug treatment or gene therapy for breast cancer, can be based on these identified gene sequences and the efficacy of any particular therapy can be monitored. The BS247-derived reagents are advantageous for detection of breast cancer due to their specificity. The reagents also provide an alternative, non-surgical diagnostic method capable of detecting early stage breast disease, such as cancer.
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                consensus polypeptide sequence
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              tissue derived cDNA contig and
                                         Claim 1; Page 105; 112pp; English.
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; ospitity of disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroidtis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number is given in the descriptor line. The gene can be used to generate fuusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. Aa206210) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 36 novel genes and their fragments (nucleic acid sequences: Aa206219-20653; amino acid sequences AA208386-Y38498) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypucleotides in a sample or by determining the presence of mutations in the new polypucleotides. Specific uses are described for each of the 36 human and a sample or by determining the presence of mutations in the new polypucleotides.
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07-JAN-1998;
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skin care product; skin flaking; dandruff; laundry detergent composition;
cleaning composition; dishwashing product; ss.
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                                                                ProHisProGlyTyrSerHisProGlyHisSerAsnAspLeuMetLeuIleLysLeuAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This DNA encodes a human keratinocyte derived protease (KDP) polypeptidd The protease is substantially similar to a sequence encoded by the inset in plasmid FERM BP-6129. The KDP polypeptide, from human keratinocytes, is specifically used in skin care products, particularly to treat or prevent skin flaking, e.g. dandruff, and in laundry detergent compositions. More generally the KDP polypeptide can be used in any cleaning composition, e.g. hard surface or dishwashing products.
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This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number is given in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AA206210) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 36 novel genes and their fragments (nucleic acid sequences: AA206219-206263; amino acid sequences AAX06219-206263; amino acid sequences AAX08386-Y38498) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypurcleotides. Specific uses are described for each of the 36 polymorleotides. based on which tissues they are most highly expressed in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel prostate derived serine protease polynucleotides and polypeptides used to modulate cellular processes \,
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/product= "PDSP-1"
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          can be used in screening assays; predictive medicine; and methods of treatment. PDSP cleaves growth factors, and can be used for the modulation of growth factor biosynthesis; generation of active peptides; regulation of cellular proliferation; degradation of growth factor binding proteins; regulation of cellular differentiation; regulation of prostate development. The PDSP polynucleotides can be used to express the protein; to detect genetic alterations in the PDSP gene; in forensic biology; and as a source of primers and probes. As serine protease have important roles in cellular processes, there exists a need for identifying novel serine protease such as the prostate derived serine protease (PDSP) of the invention. This sequence encodes the human PDSP-1 described in the
 homologs and antibodies
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                 904 TACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGACAAAGCAGGTAGAGACTCC 963
                                                                                                                                                                                                            Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand; pharmaceutical; receptor immunoadhesin; gene mapping; ss.
                                                                                    Membrane-bound protein PRO1132 encoding cDNA.
                                                                                                                                         BP
                                                                                                                                        AAZ65070 standard; cDNA; 1570
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98US-0088030.
98US-0088033.
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98US-0088734.
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10-JUN-1998;
10-JUN-1998;
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breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
adipocyte; A-peptide; factor VIIA; gene therapy; ss.
                         533
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                                                     ThrValProSerGlySerAsnGlnAspLeuGlyAlaGlyAlaGlyGluAspAlaArgSer
                        474 ACCGIGCCCTCTGGGAGCAACCAGGACCIGGGAGCTGGGGCCGGGGAAGACGCCCGGTCG
                                                                                                           GlnAlaAlaLeuLeuLeuArgProAsnGlnLeuTyrCysGlyAlaValLeuValHisPro
                                                                                                                        GlnTrpLeuLeuThrAlaAlaHisCysArgLysLysValPheArgValArgLeuGlyHis
                                                                                                                                                                                                                                     261 TrpGlyAspTyrProCysAlaArgProAsnArgProGlyValTyrThrAsnLeuCysLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor immunoadhesins, for instance, can be used as therapeutic agents the acceptor-immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences but also be useful for the preparation of PRO polypeptides, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                413
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Indels:
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Matches:
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Wood WI, Yuan J;
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Best Local Similarity:
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                                                18-AUG-1998;
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16-SEP-1998;
12-JAN-1999;
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PRO polypeptides. The PRO polypeptides are useful to detect other
PRO polypeptides, to link bloactive molecules to cells expressing
PRO polypeptides, to modulate biological activities of cells expressing
PRO polypeptides, and to detect the presence of mammalian lung, colon,
breast, prostate, rectal, cervical or liver tumours by comparing PRO
Dolypeptide expression in a cell sample to that in a control sample.
Come of the 275 sequences are also useful to stimulate the release of
tumour necrosis factor-alpha (TNF-alpha) from human blood, the
proliferation or differentiation of chondrocytes, the proliferation or
gene expression in periorte cells, the release of proteoglycans from
cartilage, the proliferation of inner ear utricular supporting cells or
of T-lymphocytes, the release of a cytokine from peripheral blood
monocytes (PBMCs), or the proliferation of endothelial cells. Some of
the PRO polypeptides may modulate glucose or free fatty acid uptake by
skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
to factor VIIA. The PRO polypeptides can be used in assays to identify
molecules involved in binding interactions. The polynucleotides encoding
PRO polypeptides can be used to generate probes, antisense RNA/DNA,
transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gao W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bloactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical
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PJ, Gurney AL, Sherwood S;
tanabe CK, Wood WI, Zhang Z;
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Matches:
Conservative:
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A, Godowski PJ, Gurne
Tumas D, Watanabe CK,
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99WO-US28564.
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2000WO-US03565
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2000WO-US04414
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10-NOV-2000; 2000WO-US30873
 2000WO-US32678
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Gerritsen ME, Goddard
Smith V, Stewart TA,
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P-PSDB; AAU12399.
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11-FEB-2000;
18-FEB-2000;
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22-FEB-2000;
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06-JAN-2000;
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09-DEC-1999;
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Percent Similarity:

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GlnAlaAlaLeuLeuLeuLeuArgProAsnGlnLeuTyrCysGlyAlaValLeuValH1sPro 100
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 Mismatches:
Indels:
                                                                       US-09-936-271B-14 (1-293) x AAS21471 (1-1570)
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Matches: Conservative: Mismatches: Indels:

2.07e-137 1608.00 100.00\$ 100.00\$

Best Local Similarity: Percent Similarity:

Query Match:

Alignment Scores:

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US-09-936-271B-14 (1-293) x AAF44216 (1-1570)

Length:

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Godowski PJ;
                                      Human; secreted and transmembrane protein; PRO; cytostatic; cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paoni NF;
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
Human PR01132 (UNQ570) nucleotide sequence SEQ ID NO:308.
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2000WO-US03565.
2000WO-US04341.
2000WO-US04414.
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99US-0141037.
99US-0143048.
99US-0144758.
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2000WO-US05841
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99US-0158663
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99WO-US28301
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                                                                             diagnostic assay; ss.
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P-PSDB; AAB65249.
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22-FEB-2000; 2
24-FEB-2000; 2
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01-DEC-1999;
16-DEC-1999;
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11-FEB-2000;
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15-SEP-1999;
08-OCT-1999;
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26-JUL-1999;
28-JUL-1999;
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                                     GINTrpLeuLeuThrAlaAlaHisCysArgLysLysValPheArgValArgLeuGlyHis
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RESULT 11 ABK28605

Sequence 1570 BP; 332 A; 485 C; 424 G; 329 T; 0 other;

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Human; ss; gene; PRO; antiinflammatory; ophthalmological; vasotropic; retinal cell injury; ocular disease; retinitis pigmentosa; macular degeneration; retinal detachment; retinal tear; retinopathy; retinal degenerative disease; macular hole; degenerative myopia; acute retinal necrosis syndrome; traumatic chorioretinopathy; Purtecher's retinopathy; oedema; ischaemic condition; retinal vision occlusion; collagen vascular disease; rhrombocytopaenic purpura; uveitis; retinal vasculitis;Eales disease; systemic lupus erythematosus; environmental trauma.
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Hark MR, Marsters SA, Pitti RM;
                                                                                                                         Human DNA59767-1489 encoding PRO1132
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ABK28605 standard; cDNA; 1570
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2000WO-US0136
2000WO-US01365
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2000WO-US01341
2000WO-US05004
2000WO-US05004
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2000WO-US05004
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99WO-US21090.
99WO-US28214.
99WO-US28313.
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Lafleur M,
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P-PSDB; AAU81966.
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18-FEB-2000; 2
22-FEB-2000; 2
24-FEB-2000; 2
02-MAR-2000; 2
15-MAR-2000; 2
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05-JAN-2000;
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Watanabe CK,
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The invention relates to promoting the survival of retinal cells, or dealying or preventing retinal cell injury or death, by contacting the retinal cells with the polypeptide such as PRO175, PRO220, PRO216, PRO216, PRO316, Promoting survival of retinal cells, or delaying or preventing retinal cell injury or death, by contacting retinal cells with PRO175, 220, 216, 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132 polypeptide Claim 33; Fig 28; 152pp; English.

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       degenerative myopia, acute retinal necrosis syndrome, traumatic chorioretinopathy acute retinal necrosis syndrome, traumatic chorioretinopathy occursion, Purtscher's retinopathy, oedema, an ischaemic condition, central or branch retinal vision occlusion, collagen vascular disease, thrombocytopaenic purpura, uveitis, retinal vasculitis, occlusion associated with Eales disease or systemic lupus erythematosus), retinal injury or environmental trauma. The retinal cell injury or death is delayed or prevented by substantially not causing anglogenesis or mitogenesis. The present sequence is a cDNA
                                                                                                                                                                                                                                                                                                                     CysGlnGlyAspSerGlyGlyProValValCysAsnGlySerLeuGlnGlyLeuValSer
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 macular hole,
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Matches:
Conservative:
Mismatches:
Indels:
 retinopathy, retinal degenerative disease,
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New secreted and transmembrane PRO nucleic acids, useful for gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                           2000WO-US04414.
2000WO-US04914.
2000WO-US05004.
2000WO-US05601.
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2001US-0828366.
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2001US-0860216.
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Gerritsen ME, Goddard
Smith V, Stewart TA,
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P-PSDB; ABU66797.
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06-JAN-2000;
11-FEB-2000;
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                                  1074 TGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCCTGCAGGGACTCGTGTCC 1133
                                                                                                                                                                                                                                                                                                                                                                 Human; PRO polypeptide; secreted and transmembrane protein;
tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
differentiation; chondrocyte; tumour; genetic disorder;
                                                                                                        cDNA encoding human PRO polypeptide #228.
                                                                                                                                                                                                                      .ACA03830 standard; cDNA; 1570 BP
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98WO-US14552.
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98WO-US18824.
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02-DEC-1999;
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Gao W;

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894 GCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAACCAAGAGCCCCCAAGTGCACTTC
                                                                                     CysGlnGlyAspSerGlyGlyProValValCysAsnGlySerLeuGlnGlyLeuValSer
                                                                                                                                                  TGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCCTGCAGGGACTCGTGTCC
                                                                        TyrProArgGlnIleAspAspThrMetPheCysAlaGlyAspLysAlaGlyArgAspSer
                                                                                                                                                                                                                                                                                                                                                                                                  Human; ss; gene; secreted protein; transmembrane protein; PRO;
inflammatory disease; organ failure; atherosclerosis; cardiac injury;
infertility; birth defects; premature aging; AIDS; blosensor;
acquired immunodeficiency syndrome; cancer; diabetic complication;
                                                                                                                                                                                                                                                                                                                                                                           Human cDNA encoding a secreted/transmembrane protein, SEQ ID 455
                                                                                                                                                                                                                                     PheThrLysTrpIleGlnGluThrIleGlnAlaAsnSer 293
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                                                                                                                                                                                                                                                                                                  ACA04251 standard; cDNA; 1570
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98WO-US19093
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14-SEP-1998;
16-SEP-1998;
17-SEP-1998;
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14-SEP-1998;
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05-JAN-1999
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                  The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for inking bloactive molecules to cells expressing PRO polypeptides, and for for identifying agonists or antagonists. The PRO polypeptides are useful for for stimulating the release of tumour necrosis factor (TMF)-alpha from human blood, for stimulating presence of tumours. The prolynucleotide sequences encoding PRO polypeptides are useful as hypidistation probes, in chromosome and presence of tumours. The polynucleotide sequences encoding PRO polypeptides are useful as hypidistation probes, in chromosome and presence of tumours. The polynucleotide sequences encoding PRO polypeptides are useful as hypidistation probes, in chromosome and preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the genetic analysis of individuals with genetic disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs encoding the human PRO polypeptides of the invention.

Note: The sequence data for this patent was obtained in electronic sequata uspto.gov/psipsDIDEntry.html.
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Matches:
Conservative:
Mismatches:
Indels:
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Claim 2; Fig 455; 660pp; English.
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25-MAY-2001;
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The invention relates to an isolated nucleic acid comprising, or which is at least 80% identical to, or the full-length coding sequence of, any of the 275 nucleotide sequences, encoding the corresponding PRO polypeptide (one of 275 secreted or transmembrane proteins). The nucleic acid further comprises the full-length coding sequence of the DNA deposited cunder American Type Culture Collection (ATCC) accession number in a list given in the specification. Also included are vectors and host calls for producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO extracellular domains and mature sequences, methods of detecting PRO proteins, methods for stimulating the release of TNF-alpha (tumour necrosis factor alpha) from human blood, (and the proliferation of differentiation of chondrocyte cells, the release of proliferation of, or gene expression in pericyte cells, the release or proteoglycans from cartilage, proliferation of inner ear urticular supporting cells, the proliferation of T-lymphocyte cells, the release of a cytokine from peripheral blood mononuclear cells, the release of proliferation of endothelial cells), a method for modulating the uptake of glucose or free fatty acid (FFA) by skeletal muscle cells, or the differentiation of adippocyte cells, a method for modulating the proliferation of adippocyte cells, a method for detecting the proliferation of adippocyte cells, a method for detecting the proliferation of adippocyte cells, a method for detecting the proliferation of adippocyte cells, a method for detecting the proliferation of adippocyte cells, a method for detecting the proliferation of adippocyte cells, a method for detecting the proliferation of adippocyte cells, a method for detecting the proliferation of adippocyte cells, a method for detecting the problem and of the differentiation of adippocyte cells, a method for detecting the problem and gene mapping, and in generating antisense RNA probebs, in chromosome and gene mapping, and in generating antisense RNA probebs, or bNA The p
                                                                                                                                                                                                                                                  New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature
                                                          Gao
                                                    DeForge L, Desnoyers L, Filvaroff E, Ga
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biosensors or bioreactors. Both are useful in tissue typing the present sequence encodes a PRO protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1570 BP; 332 A; 485 C; 424 G; 329 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Fig 455; 659pp; English.
                                                    Beresini M,
                                                                                                                                                                                                                                                                                                                                          aging, AIDS, or cancer
(GETH ) GENENTECH INC.
                                                                                                            Stewart TA,
                                                                                                                                                                WPI; 2003-331925/31.
P-PSDB; ABU67073.
                                                    Baker KP, Ber
Gerritsen ME,
                                                                                                            Smith V,
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Conservative: Mismatches: Indels: Length: Matches: US-09-936-271B-14 (1-293) x ACA04251 (1-1570) Gaps: 2.07e-137 1608.00 100.00% 100.00% Similarity: Percent Similarity: Best Local Similarit Alignment Scores: Query Match: Pred. No.: QY

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61 AspaspSerSerSerArgIleIleAsnGlySerAspCysAspMetHisThrGlnProTrp 80

| 534 GATGACAGCAGCAGCATCATCAATGGATCCGACTGCGATATGCACCCAGCCGTGG 593 | PF | | 2002US-0140808 | |
|--|--|--|--|----------|
| 81 GlnalaalaLeuLeuLeuArgProAsnGlnLeuTyrCysGlyAlaValLeuValHisPro 100 | PR | | 97WO-US05230 98WO-US12456 98WO-US14552 | |
| 101 GlnfrpLeuLeuthralaalaHisCysArgLysLysValPheargValargLeuGlyHis 120 | ያ ማ ማ ማ ጃ ጃ ጃ ጃ ጃ | | 98WO-US18824 98WO-US18824 98WO-US19093 98WO-US19094 | |
| 121 TyrSerLeuSerProValTyrGluSerGlyGlnGlnWetPheGlnGlyValLysSerIle 140 | 7 | | 98WO-US19330 98WO-US19437 98WO-US19437 98WO-US21141 | |
| 141 ProHisProGlyTyrSerHisProGlyHisSerAsnAspLeuMetLeuIleLysLeuAsn 160 | 7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 | | 98WO-USZZ991 98WO-USZ2992 98WO-USZ4855 98WO-USZ5108 | |
| 161 ArgargileargProThrLysAspValargProileasnValSerSerHisCysProSer 180 | 7 7 7 7 7 | | 99WO-USUGIO 99WO-USO5028 99WO-USO5190 99WO-USO8615 | |
| 181 AlaGIyThrLysCysLeuValSerGlyTrpGlyThrThrLysSerProGlnValHisPhe 200 | 7 7 7 7 7 7 7 7 7 1 | | 99WO-USIO/33 99WO-USI2255 99WO-US20111 99WO-US20594 | |
| 201 ProLysValLeuGinCysLeuAsnileSerValLeuSerGinLysArgCysGluAspAla 220 | 7 7 7 7 7 | | 99WO-USZU944 99WO-USZ109C 99WO-USZ1547 | |
| 221 TyrProArgGlnIleAspAspThrMetPheCysAlaGlyAspLysAlaGlyArgAspSer 240 | 7 9 9 9 E | | 99WO-US28313 99WO-US28313 99WO-US28301 | |
| 241 CysGlnGlyAspSerGlyGlyProValValCysAsnGlySerLeuGlnGlyLeuValSer 260 | 7 7 7 7 X X X X X | | 99WO-US28551 99WO-US28551 99WO-US28565 | |
| 261 TrpGlyAspTyrProcysAlaArgProAsnArgProGlyValTyrThrAsnLeuCysLys 280 | ያ ያ ያ ማ ያ ያ | | 99WO-US30911 99WO-US30910 99WO-US30720 | ::22. |
| 281 PhethriysTrpileGlnGluThrileGlnAlaasnSer 293 | 7 7 7 8 8 | | 2000WO-US31274 2000WO-US31274 2000WO-US00215 | 1121. |
| ESULT 14 BX89368 D ABX89368 standard; CDNA; 1570 BP. | 7 7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 | | 2000WO-US0355 2000WO-US03565 2000WO-US04341 | :.: :.:_ |
| 100 | 4 64 64 6 | | 2000WO-US04914 2000WO-US04914 2000WO-US05004 | |
| 13-MAY-2003 (ILIST entry) DNA encoding novel secreted and transmembrane protein PRO1132. | 7 4 4 4 7 5 5 5 5 | | 2000WO-US05841 | |
| an; PRO; hypertrophy of neonatal, heart; angiogenesis; wound healing; diac insufficiency disorder; cancer; tumour; immune response; enal cortical capillary endothelial growth; c-fos induction; cular endothelial growth factor inhibition; VEGF inhibition; cular endothelial growth inhibitor; T-lymbhcovtes stimulation; | 7 7 7 7 7 7 8 8 8 8 8 8 | | 2000WO-USOGBR 2000WO-USO737 2000WO-USO757 2000WO-USO8439 2000WO-USO8439 | : |
| retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kidney disorder; mammalian kidney mesangial cell proliferation; Berger disease; dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis; gene; ss. | PR PR PR | 22-MAY-2000; 30-MAY-2000; 02-JUN-2000; 28-JUL-2000; 11-AUG-2000; | 2000WO-US14042. 2000WO-US14941. 2000WO-US15264. 2000WO-US20710. 2000WO-US2031. | ~:-:-: |
| Homo sapiens. US2003017563-A1. | X | | 2000MO-US23328 2000MO-US23328 2000MO-US30953 2000MO-US30873 | |
| 23-JAN-2003. | 7 7 8 8 8 | | 2000WO-US326/2 2000WO-US3495/ 2001WO-US0652 | |

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Claim 2; Fig 455; 659pp; English.
2001WO-US06666
                            2001WO-US21066
2001WO-US21735
                                      2000US-0747259
                                            2001US-0796498
                                                  200105-0802706
                                                        2001US-0808689
                2001WO-US19692
                      2001WO-US20116
                                                                              2001US-0854280
                                                             2001US-0816744
                                                                         2001US-0854208
                                                                                                                                                       2001US-0028072
                                                                                               2001US-0866034
                                                                                                                                                                            Beresini M, Dei
ME, Goddard A,
Stewart TA, Tum
                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                  WPI; 2003-148238/14.
P-PSDB; ABU59878.
                                                                                                                                                                                  Gerritsen ME,
               20-JUN-2001;
22-JUN-2001;
                                      20-DEC-2000;
28-FEB-2001;
                                                 09-MAR-2001;
14-MAR-2001;
                                                             22-MAR-2001;
                                                                  05-APR-2001;
10-MAY-2001;
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19-DEC-2001;
                                                                             10-MAY-2001;
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                                                                                         25-MAY-2001;
                                                                                               25-MAY-2001;
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                                                                                                                     19-JUN-2001;
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                                                                                                                                           09-AUG-2001;
                                                                                                                                      36-AUG-2001
                                                                                                                                                                                                                                     treatments
                                                                                                                                                                            Baker KP,
                                                                                                                                                                                        Smith V,
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3 Gao Filvaroff E, Ga L, Sherwood S; od WI, Zhang Z; Deforge L, Desnoyers L, Filvar A, Godowski PJ, Gurney AL, She Tumas D, Watanabe CK, Wood WI, Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in consuperative molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus constain cardiac insufficiency disorders. PRO154 and PRO1186 stimulate adrenal cortical capillary endothelial growth, and PRO536, PRO943, PRO943, PRO826, PRO1068 or PRO535, PRO826, PRO1367 induce crics in endothelial growth, and are thus useful for treating conditions or disorders where angiogenesis would be cheficial, e.g. wound healing and antagonist of this polypeptide are useful for treating conditions tumours. PRO812 inhibits vascular cells useful for treating conditions tumours. PRO812 inhibits vascular cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO1068, PRO1184, PRO1346 and are this polypeptide are cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO1068, PRO1068, PRO1184, PRO1346 and PRO1375 stimulated proliferation of stimulated T-lymphocytes and are therapeutically useful for rehancing immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival portiferation of disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813 cand therefore are useful for treating kidney disorders associated with dermatitis, herpetiformis or conherced and PRO1312, pRO1192 and PRO1310, pRO814, PRO81312, PRO1312, and PRO8131, induce the complication and/or redifferentiation of chondrocytes in culture and ere thus useful for treating sports injuries, and arthritis. This

| SS X | sednence | encodes a 1570 BP; | novel human 332 A; 485 C; | PRO protein. 424 G; 329 T; 0 c | other; | |
|---|--|--------------------------|---|--|------------------------------|-------|
| Alig Pred Scor Perc Best Quer DB: | nment Sco 1. No.: re: sent Simil . Local Si. Y Match: | res: arity: nilari | 2.07e-137 1608.00 100.008 100.008 100.008 | Length: Matches: Conservative: Mismatches: Indels: | 1570 293 0 0 | |
| 0-SO | 09-936-2715 | B-14 (1-29 | 33) x ABX89368 | -15 | | |
| Qy | 1 | MetAlaThrA] | laArgProProTi | rpMetTrpValLeuCysAla | AlaLeuIleThrAlaLeuLeu | 7 |
| qq | 354 | GCT | PAGACCCCCCTC | GATGTGGGTGCTCT | CTGATCACAGCCTTGCT | 413 |
| oy op | 21 | LeuGlyVal1 | ChrGluHisV | 7alLeuAlaAsnAsnAspValS | SerCysAspHisProSerAsn | 473 |
| ΟŸ | 4 | Thrval | serGlySerAsnGl | euGlyAlaGly | NaGlyGluAspAlaArgS | 9 |
| qq | 474 | ACCGTGCCCTC | TEGGAGCAACC | AGGACCTGGGAGCTGGGG | GCCGGGGAAGACGCCCGGTCG | 533 |
| Qγ | 61 | AspAspSer | SerSerArgllell | eAsnGlySerAspCy | sAspMetHisThrGlnProTrp | 80 |
| qq | 534 | GATGACAGC | AGCAGCCGCATCAT | CAATGGATCCGACTG | SCACACCCAGCCGTG | 593 |
| Qy | 81 | GlnAlaAlaLe | euLeuLeuArgPr | OAsnGlnLeuTyrCys | GlyAlaValLeuValHisPro | 10 |
| qq | 594 | CAGGCCGCG | GTTGCTAAGGCC | CAACCAGCTCTACTGC | rerregrecarce | 653 |
| QY | 101 | GlnTrpLeuLe | euThrAlaA] | aHisCysArgLysLysValF | PheArgValArgLeuGlyHis | 120 |
| QQ | 654 | CAGIGGCIG | rcaceecee | AAGAAAGTT | AGAGTCCGTCTCGGCCA | 713 |
| ٥y | 121 | TyrSerLeus | SerProvalTyr | GluSerGlyGlnGlnMetF | tPheGlnGlyValLysSerIle | 14 |
| q a | 714 | ACTCCC | CACCAGTTTAT | TGGG | GTCAAATCCAT | 773 |
| oy 4 | | ProHisPro | roGlyTyrSerHisPr | ProGlyHisSerAsnAspLeuMetLeu | LeuMetLeuIleLysLeuAsn | 16 |
| a d | | | | Teeccaciciaaceacc | Algerealcanaciena | 6 |
| Oy Dp | 161 834 | ArgargileargF | eargprothrlysaspvalargp | spValArgProIleAsnVal | /alSerSerHisCysProSer | 180 |
| Qy | 181 | AlaGlyThr | ysLeuVal | rGlyTrpGlyThrThr | SerProGlnValHisPh | 200 |
| qa | 894 | _გ | GACAAAGTGCTTGGTGTC | TCTGGCTGGGGGACAACCAAG | AGCCCC | 953 |
| Qy | 201 | ProLysValLeuG | IncysLe | uAsnIleSerValLeuSerC | GlnLysArgCysGluAspAla | 220 |
| QQ | 954 | CCTAAGGTC | AGTGCTI | CGTGCTAAGI | TGCGAGGATGC | 1013 |
| Qy | 221 | TyrProArgGlnIle | JGlnIleAspAspThrMet | Phecy | SAlaGlyAspLysAlaGlyArgAspSer | 240 |
| qa | 1014 | TACCCGAGA | ACAGATAGATGACAC | TTCTG | - () | 1073 |
| Oy | 241 | CysGlnGly | AspSerGlyGly | ProvalvalCysAsnGlyS | SerLeuGlnGlyLeuValSer | . 260 |
| qq | 1074 | CCAGG | GATTCTGGGGG | CTGCAATGG | AGGACTCGTGT | 1133 |
| Qy | 261 | TrpGlyAsp? | TyrProCysAlaAr | gProAsnArgProG1 | yValTyrThrAsnLeuCysLys | 280 |
| qa | 1134 | GGGGAGAT | raccerrerec | scccaacagaccgg | TACACGAACCTCTGCAA | 1193 |
| QY | | PheThrLys | heThrLysTrpIleGlnGluThrI | nrIleGlnAlaAsnSer | 90 | |
| qa | 1194 | TTCACCAAC | STGGATCCAGGAAAC | TCCAGGCCAACT | 1232 | |

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PPRESENTATION OF THE PRESENTATION OF THE PRESE
                                                                                                                                                                           Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth; c-fos induction; vascular endothelial growth inhibition; VEGF inhibition; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinal survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kidney disorder; mammalian kidney mesangial cell proliferation; Berger disease; chondrocyte redifferentiation; sports injury; arthritis; PCR; primer; ss.
                                                                                                                                                 Human secreted or transmembrane protein related PCR primer #56.
                                            ABX80318 standard; DNA; 1570 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-US20069.
98WO-US19330.
98WO-US19437.
98WO-US21141.
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99WO-US00106.
99WO-US05028.
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                                                                                                              28-APR-2003 (first entry)
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11-FEB-2000;
24-FEB-2000;
24-FEB-2000;
24-FEB-2000;
02-MAR-2000;
10-MAR-2000;
115-MAR-2000;
20-MAR-2000;
20-MAR-2000;
20-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-NOV-1999;
01-DEC-1999;
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16-DEC-1999;
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22-MAY-2000;
30-MAY-2000;
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05-JAN-1999;
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15-SEP-1999;
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29-JUN-2001;
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                                                                             ABX80318;
            RESULT 15
ABX80318
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970S-065186P
970S-065311P
970S-065311P
970S-06770P
980S-075945P
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          17.0CT-1997;
12.NOV-1997;
13.NOV-1997;
25.PEB-1998;
20.MAR-1998;
28.MAY-1998;
28.MAY-1998;
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PJ; Godowski P Paoni NF; Wood WI; Eaton Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Zhang Z;

WPI; 2003-247083/24.

Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer treatments

Example 99; Page 259; 648pp; English.

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO

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Sequence 1570 BP; 332 A; 485 C; 424 G; 329 T; 0 other;

lovel human PRO polypeptides.

| | . Length: | Matches: | Conservative: | Mismatches: | Indels: | Gaps: |
|-------------------|------------|----------|---------------------|------------------------|--------------|-------|
| | 2.07e-137 | 1608.00 | 100.00% | 100.00% | 100.00% | 25 |
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1570 293

US-09-936-271B-14 (1-293) x ABX80318 (1-1570)

| ò á | 1 | MetAlaThrAlaArgProProTrpMetTrpValLeuCysAlaLeuIleThrAlaLeuLeu |
|-----|-------|--|
| 3 | * 0 0 | AIGGCIACAGCAAGACCCCCCIGGAIGIGGGIGCICIGIGCICIGAICACAGCCIIGCII 413 |
| δy | 21 | LeuGlyValThrGluHisValLeuAlaAsnAsnAspValSerCysAspHisProSerAsn 40 |
| qq | 414 | CTGGGGGTCACAGAGCATGTTCTCGCCAACAATGATGTTTCCTGTGACCACCCTCTAAC 473 |
| οy | 41 | ThrValProSerGlySerAsnGlnAspLeuGlyAlaGlyAlaGlyGluAspAlaArgSer 60 |
| qq | 474 | ACCGTGCCCTCTGGGGGGGAACCAGGACCTGGGGGCCGGGGAAGACGCCCGGTCG 533 |
| Oy | 61 | AspAspSerSerArgIleIleAsnGlySerAspCysAspWetHisThrGlnProTrp 80 |
| qq | 534 | GATGACAGCAGCAGCATCATCAATGGATCCGACTGCGATATGCACACCCAGCCGTGG 593 |
| Οy | 81 | GlnAlaAlaLeuLeuLeuArgProAsnGlnLeuTyrCysGlyAlaValLeuValHisPro 100 |
| q | 594 | CAGGCCGCGCTGTTGTTTTTTTTTTTTTTTTTTTTTTTT |
| δy | 101 | GlnTrpLeuLeuThrAlaAlaHisCysArgLysLysValPheArgValArgLeuGlyHis 120 |
| q | 654 | CAGTGGCTGCTCACGCCCCCCACTGCAGGAAGAAGTTTTCAGAGTCTGTCGGCCCAC 713 |
| Qy | 121 | TyrSerLeuSerProValTyrGluSerGlyGlnGlnMetPheGlnGlyValLysSerIle 140 |
| qq | 714 | TACTCCCTGTCACCAGTTTATGAATCTGGGCAGCAGATGTTCCAGGGGGTCAAATCCATC 773 |
| ογ | 141 | ProHisProGlyTyrSerHisProGlyHisSerAsnAspLeuMetLeuIleLysLeuAsn 160 |
| qa | 774 | CCCCACCCTGGCTACTCCCACCCTGGCCACTCTAACGACCTCATGCTCATCAACTGAAC 833 |
| ΟŸ | 161 | ArgArgIleArgProThrLysAspValArgProIleAsnValSerSerHisCysProSer 180 |

| да , | 834 181 894 | 834 AGAAGAATTCGTCCCACTAAAGATGTCAGACCCATCAACGTCTCCTCTCATTGTCCCTCT 893 181 AlaGlyThrLysCysLeuValSerGlyThrThrLysSerProGlnValHisPhe 200 111111111111111111111111111111111111 |
|----------|-------------------|--|
| QY Db | 201 | ProLysValLeuGlnCysLeuAsnIleSerValLeuSerGlnLysArgCysGluAspAla 220 |
| Qy | 221 | TyrproargGln1leaspaspThrMetPheCysalaGlyaspLysAlaGlyargAspSer 240 |
| da | 241 | CysGlnGlyAspSerGlyGlyProValValCysAsnGlySerLeuGlnGlyLeuValSer 260 |
| Qy | 261 | TrpGlyAspTyrProCysAlaArgProAsnArgProGlyValTyrThrAsnLeuCysLys 280 |
| Qy | 281 | 281 PheThrLysTrp11eGlnGluThr11eGlnAlaAsnSer 293 |

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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                       OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                             569978 seqs, 220691566 residues
                                                                                                                                                                                                                                                                                   0.5
7.0
7.0
                                                                                                                                                                                                                                                                             Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                 BLOSUM62
                                                                                                                                                                                      Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                             Run on:
```

Listing first 45 summaries

Post-processing: Minimum Match 0% Maximum Match 100%

Command line parameters:
-MODEL-france+_p2n, model - DEV=Xlp
-VG=/Cgn2_1/USPTO_spool/US09936271/runat_04082003_104246_25727/app_query.fasta_1.455
-VG=/Cgn2_1/USPTO_spool/US09936271/runat_04082003_104246_25727/app_query.fasta_1.455
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-LOOPEXT=0 - UNITS=bits - START=1 - END=-1 - MATRIX=blosum62 - TRR_MINED 0 - ALIGN=15
-LIST=45 - DOCALIGH-200 - THR_SCORE=-pct - THR_MINED 0 - ALIGN=15
-LOCAL - OUTFMT-PtO - NORM-ext - HEAPSTIZE=500 - MINIEN=0 - MAXIEN=200000000
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-NO_MMAP - LARGEQUERY - NGG_SCORES=- OWAIT - DSPBLOCK-100 - LONGING .
-DEV_TIMEOUT=120 - WARN_TIMEOUT=30 - THREADS=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELDEXT=7

Issued_Patents_NA:* Database

/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/Packfiles1.seq:* /cgn2_6/ptodata/1/ina/5A_COMB.seq:*/cgn2_6/ptodata/1/ina/5B_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

2, Appli 2, Appli 2, Appli 1, Appli 94, Appl Sequence 308, App Description Sequence Seq US-09-996-243-308 US-08-824-874-2 US-09-210-084-2 US-09-280-116-1 US-09-280-116-1 US-09-439-136-24 US-09-386-642-10 US-09-205-258-247 US-08-944-483-8 US-08-944-483-8 SUMMARIES DB Query Match Length 999.2 999.2 999.2 445.1 441.7 440.6 440.6 40.5 100.0 652.5 652.5 650.5 650.5 Score 1403 Result ږ چ

, App Appli Appli Appli

| 186 | Sequence 2, Appli | , 5 | , · | | | 7 | • | 171, | 171, | 171, | Sequence 171, App | 17 | 09 | 6 | 22 | Sequence 225, App | 22 | 32 | 32 | 32 | 30 | 1, | Ţ | 1, | 3, | 1, | 'n | 1 | ť | 20 | 17 | 17 |
|----------|-------------------|--------------|----------|----------|----------|----------|----------|-------------------|----------|--------------|-------------------|---------|------|---------|---------|-------------------|----------|---------|---------------|-----------------|--------|-------|-----------------|-------|-----------------|----------|------------------|------------|-------------|------------|---------------|-------------------|
| -09-205- | -09-025-059-2 | -09-008-Z/IA | -020-60- | -08-744- | -09-102- | -09-261- | -696-80- | US-09-020-956-171 | -080-60- | -09-439-313- | -09-352 | -09-232 | -60- | 986-60- | -09-439 | -09 - 35 | -09-232- | 9-313-3 | -09-352-616A- | -09-232-149A-32 | -09-20 | -146- | US-09-154-344-1 | -188 | US-08-930-188-3 | -us96-04 | PCT-US96-04294-3 | 38-897-340 | -09-252-329 | -280-116-2 | -09-020-956-1 | US-09-030-607-173 |
| 2 4 | 4. | 4. v | 4. | 1 | 1 2 | 1 3 | 1 4 | 8 3 | 8 | 8 4 | 8 4 | 8 4 | 7 4 | 9 | 4 4 | 4 4 | 4 4 | 5 4 | 5 4 | 5 4 | 6 3 | 6 2 | 6 2 | 9 | 9 | 9 | 9 5 | 6 2 | 9 | 4 4 | 5 | 5 |
| 1292 | 131 | 20.0 | 9.0 | 87 | 87 | 87 | 87 | 124 | 124 | 124 | 124 | 124 | 103 | 104 | 121 | 121 | 121 | 121 | 121 | 121 | 96 | 86 | 86 | 108 | 108 | 108 | 108 | 138 | 138 | 136 | 126 | 126 |
| 4 | 40. | 30.0 | 9.0 | 39. | 39. | 39. | m | 39. | 39. | n | m | 39. | m | 39. | 38. | m | 38. | 38. | 38. | 38. | 38. | 38. | 38. | 38. | 38 | 38. | 38. | 36. | m | 36. | 36 | 36. |
| 650.5 | 0.00 | 0.89.0 | 638.5 | 638 | 638 | 638 | 638 | 638 | 638 | 638 | 638 | .889 | 635 | 632.5 | 620 | 620 | 620 | 620 | 620 | 620 | 612.5 | 612.5 | 612.5 | 612.5 | 612.5 | 612.5 | 612.5 | 290 | 290 | 585 | 582.5 | 582.5 |
| 13 | 14 2 | Ω, T, | 9! | 1.7 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 59 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |
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ALIGNMENTS

| R | RESULT 1 IS-09-996-243-308 | |
|-------|---|---|
| · · · | Sequence 308, Application US/09996243 | |
| | FACELL NO. 04/0623 GENERAL INFORMATION: | |
| •• | APPLICANT: Ashkenazi, Avi J. | |
| •• | APPLICANT: Baker, Kevin P. | |
| •• | | |
| •• | | |
| •• | APPLICANT: Eaton, Dan L. | |
| • | APPLICANT: Ferrara, Napoleone | |
| •• | APPLICANT: Fong, Sherman | |
| ٠. | APPLICANT: Gerber, Hanspeter | |
| • | | |
| •• | | |
| ٠. | APPLICANT: Godowski, Paul J. | |
| •- | | |
| • | APPLICANT: Gurney, Austin L. | |
| •• | APPLICANT: Kljavin, Ivar J. | |
| •- | APPLICANT: Napier, Mary A. | |
| ٠. | APPLICANT: Pan, James | |
| •• | APPLICANT: Paoni, Nicholas F. | |
| •• | APPLICANT: Roy, Margaret Ann | |
| ٠. | APPLICANT: Stewart, Timothy A. | |
| •• | APPLICANT: Tumas, Daniel | |
| •- | APPLICANT: Watanabe, Colin K. | |
| •- | APPLICANT: Williams, P. Mickey | |
| •• | 7111 | |
| •• | APPLICANT: Zhang, Zemin | |
| •• | TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and | × |
| •• | TITLE OF INVENTION: Acids Encoding the Same | |
| •- | FILE REFERENCE: P2730P1C13 | |
| •- | CURRENT APPLICATION NUMBER: US/09/996,243 | |
| •- | T FILING DATE: 2001 | |
| •- | | |
| •• | PRIOR FILING DATE: 1997-06-16 | |

Nucleic

PPLICATION NUMBER: 60/088025 ILING DATE: 1998-06-04 LING DATE: 1998-06-04 PLICATION NUMBER: 60/088326 APPLICATION NUMBER: 60/066770 FILING DATE: 1997-11-24 APPLICATION NUMBER: 60/088029 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088742 FILING DATE: 1998-06-10 FILING DATE: 1998-06-11
APPLICATION UNMBER: 60/089105
FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089440 NUMBER: 60/062250 APPLICATION NUMBER: 60/075945 APPLICATION NUMBER: 60/078910 CATION NUMBER: 60/083322 APPLICATION NUMBER: 60/084600 APPLICATION NUMBER: 60/087106 APPLICATION NUMBER: 60/087759 60/088026 APPLICATION NUMBER: 60/088028 ION NUMBER: 60/088030 PLICATION NUMBER: 60/088033 PLICATION NUMBER: 60/088202 APPLICATION NUMBER: 60/088212 APPLICATION NUMBER: 60/088217 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088655 FILING DATE: 1998-06-09 APPLICATION NUMBER: 60/088734 APPLICATION NUMBER: 60/088738 60/088810 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088824 APPLICATION NUMBER: 60/088826 60/088858 APPLICATION NUMBER: 60/088876 APPLICATION NUMBER: 60/065311 APPLICATION NUMBER: 60/087607 PLICATION NUMBER: 60/087609 60/087827 APPLICATION NUMBER: 60/088021 FILING DATE: 1998-06-04 PLICATION NUMBER: 60/088167 1998-06-05 60-90-866 998-05-28 1998-06-02 998-06-03 1998-06-04 998-06-04 998-06-05 998-06-10 998-05-07 998-06-02 998-06-04 998-06-04 1998-06-05 998-02-25 998-03-20 998-06-02 998-06-11 1997-11-13 998-04-2 -90-866 -90-866 -90-866 -90-866 FILING DATE: 1998-06 APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: LING DATE: LING DATE: LING DATE: LING DATE: LING DATE: ILING DATE: LING DATE: PRRICK RELIGIOR PRESENTATION PRESENTATION PROPERTY OF PRESENTATION PROPERTY OF PRESENTATION PROPERTY OF PRESENTATION PRESE PRIOR PRIOR

APPLICATION NUMBER: 60/089532 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089538 60/090246 60/090349 APPLICATION NUMBER: 60/090429 60/090435 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090444 APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090472 60/090535 APPLICATION NUMBER: 60/090540 APPLICATION NUMBER: 60/090542 60/090862 APPLICATION NUMBER: 60/089514 CATION NUMBER: 60/089599 APPLICATION NUMBER: 60/089908 APPLICATION NUMBER: 60/089948 60/090252 60/090355 APPLICATION NUMBER: 60/090557 APPLICATION NUMBER: 60/090678 60/089598 60/089653 60/089801 APPLICATION NUMBER: 60/089907 60/089947 60/089952 APPLICATION NUMBER: 60/090431 60/090254 1998-06-16 1998-06-18 1998-06-19 1998-06-24 FILING DATE: 1998-06-24 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-26 1998-06-16 1998-06-17 1998-06-17 1998-06-17 1998-06-18 1998-06-18 1998-06-22 1998-06-22 1998-06-23 1998-06-24 1998-06-25 998-06-25 1998-06-24 1998-06-24 998-06-2 1998-06-1 -90-866 -90-866 -90-8661 FILING DATE: 1998-06 APPLICATION NUMBER: FILING DATE: 1998-06 APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: CATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE:

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1073
                                                                                                    1134 TGGGGAGATTACCCTTGTGCCCGGCCCAACAGACCGGGTGTCTACACGAACCTCTGCAAG 1193
 954 CCTAAGGTCCTCCAGTGCTTGAATATCAGCGTGCTAAGTCAGAAAAGGTGCGAGGATGCT 1013
                                Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-936-271B-14 (1-293) x US-08-824-874-2 (1-1476)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.0
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMBUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESD for Windows Version 2.(
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATE...
ATORNES DATE:
ATORNEY AGENT INFORMATION:
NAME: B111ings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
""" PPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                               US-08-824-874-2; Sequence 2, Application US/08824874; Patent No. 5962300; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.12e-159
1595.00
99.66%
99.66%
29.19%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGIH: 1476 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIBRARY: KERANOT02
CLONE: 820694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: C. COUNTRY:
                                                                                                                                                                          261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlnAlaAlaLeuLeuLeuArgProAsnGlnLeuTyrCysGlyAlaValLeuValHisPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProHisproGlyTyrSerHisproGlyHisSerAsnAspLeuMetLeuIleLysLeuAsn 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AlaGlyThrLySCySLeuValSerGlyTrpGlyThrThrLySSerProGlnValHisPhe 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            774 CCCCACCCTGGCTACTCCCACCCTGGCCACTCTAACGACCTCATGCTCAAACTGAAC 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AspAspSerSerSerArgIleIleAsnGlySerAspCysAspMetH1sThrGlnProTrp 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetalaThralaArgProProTrpMetTrpValLeuCysAlaLeulleThrAlaLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 LeuGlyValThrGluHisValLeuAlaAsnAsnAspValSerCysAspHisProSerAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-936-271B-14 (1-293) x US-09-996-243-308 (1-1570)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                          PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/09154
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR PAPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR APPLICATION NUMBER: 60/091636
PRIOR APPLICATION NUMBER: 60/091636
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/090863
                                                                                                                                                                                                                                                                                                                                                                             9.79e-161
1608.00
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100.00%
                 LING DATE: 1998-06-26
                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               534
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oGlnTrpLeuLeuThrAlaAlaHisCysArgLysLysValPheArgValArgLeuGlyHi 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GlnAlaAlaLeuLeuLeuArgProAsnGlnLeuTyrCysGlyAlaValLeuValHisPr 100
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293
0
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1
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches:
Indels:
                                                                  COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                       FILING DATE:
CLASTPICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
ATORNEY/AGENT INFORMATION:
NAME: Bilings, Lucy J.
REGISTRATION NUMBER: 36,749
REFENCE/DOCKET NUMBER: 9F-0252 US
TELECOMMUNICATION:
TELEPHONE: 415-955-0555
                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
                                                                                                                                                                                                                                                                                                                                                                                                       2.12e-159
1595.00
99.66%
99.66%
                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                    415-845-4166
                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Palo Alto
                                                                                                                                                                                                                                                                                                                                      MEDIALL
LIBRARY: KERAN
LIBRARY: 820694
                                                                                                                                                                                                                                                                                                                      TOPOLOGY: line
                      USA
                                94304
            S
                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores
                                                                                                                                                                                                                                                       TELEFAX:
                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                     US-09-210-084-2
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                                 277 ATGGCTACAGCAAGACCCCCCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTT 336
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            MetalaThralaArgProProTrpMetTrpValLeuCysAlaLeuIleThrAlaLeuLeu
                                                        LeuGlyValThrGluHisValLeuAlaAsnAsnAspValSerCysAspHisProSerAsn
                                                                                                                                                  AspAspSerSerSerArgIleIleAsnGlySerAspCysAspMetHisThrGlnProTrp
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09210084
Patent No. 6197311
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 5
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| SEQU | 9-764-762-2 nment Scores: | 2.12e-159 1595.00 1arity: 99.66% imilarity: 99.66% | Indels: Gaps: 9-764-762-2 (1-1476) | Qy 1 MetalaThralaArgProProFrpWetTrpValLeuCysAlaLeuIleThrAlaLeuLeu 20 | Qy 21 LeuGlyValThrGluHisValLeuAlaAsnAspValSerCysAspHisProSerAsn 40 | Oy 41 ThrValProSerGlySerAsnGlDAspLeuGlyAlaGlyAlaGlyGluAspAlaArgSer 60 | Oy 61 AspAspSerSerArgileileAsnGlySerAspCysAspMetHisThrGlnProTrp 80 | Qy 81 -GInAlaAlaLeuLeuLeuArgProAsnGlnLeuTyrCysGlyAlaValLeuValHisPr 100 | Qy 100 oGlnTrpLeuLeuThrAlaAlaHisCysArgLysUsValPheArgValArgLeuGlyHi 120 | Oy 120 sTyrSerLeuSerProValTyrGluSerGlyGlnGlnMetPheGlnGlyValLysSerIl 140 | Qy 140 eProHisProGlyTyrSerHisProGlyHisSerAsnAspLeuMetLeuIleLysLeuAS 160 | Qy 160 nArgArgIleArgProThrLysAspValArgProIleAsnValSerSerHisCysProSe 180 | Qy 180 rAlaGlyThrLySCySLeuValSerGlyTrpGlyThrThrLySSerProGlnValHiSPh 200 | Qy 200 eProLysValLeuGlnCysLeuAsnIleSerValLeuSerGlnLysArgCysGluAspAl 220 | Qy 220 aTyrProArgGlnIleAspAspThrMetPheCysAlaGlyAspLysAlaGlyArgAspSe 240 - | Qy 240 rCysGlnGlyAspSerGlyGlyProValValCysAsnGlySerLeuGlnGlyLeuValSe 260 | Qy 260 rTrpGlyaspTyrProCysalaArgProAsnArgProGlyvalTyrThrAsnLeuCysLy 280 | Qy 280 sPheThrLysTrplleGlnGluThrlleGlnAlaAsnSer 293 |
|------|---|---|---|---|---|---|--|---|--|--|---|---|---|--|---|---|---|---|
| | OY 160 nArgArg1leArgProThrLysAspValArgProIleAsnValSerSerHisCysProSe 180 | Qy 180 rAlaGlyThrLysCysLeuValSerGlyTrpGlyThrThrLysSerProGlnValHisPh 200 | Qy 200 eProLysValLeuGlnCysLeuAsnIleSerValLeuSerGlnLysArgCysGluAspAl 220 | Qy 220 aTyrProArgGlnIleAspAspThrMetPheCysAlaGlyAspLysAlaGlyArgAspSe 240 | Qy 240 rcysGlnGlyAspSerGlyGlyProValValCySAsnGlySerLeuGlnGlyLeuValSe 260 | Qy 260 rTrpGlyAspTyrProCysAlaArgProAsnArgProGlyValTyrThrAsnLeuCysLy 280 | Qy 280 sPheThrLysTrpIleGlnGluThrIleGlnAlaAsnSer 293 | RESULT 4 US-09-764-762-2 ; Sequence 2, Application US/09764762 batcat No. 6477016 | GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Hillman, Jennifer L. Lal, Preeti | TITLE OF INVENTION: NOVEL KALLIKREIN NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS: 5 ADDRESSEE: Incyte Pharmaceuticals, Inc. | | | CURRENT APPLICATION DATA: CURRENT APPLICATION DATA: APPLICATION UNMBER: US/09/764,762 | FILTING DATE: 10 Jan 2001 CLASSIFICATION: CHROMD> PRIOR APPLICATION DATA: APPLICATION UNDBER: FILTING DATE: CLASSIFICATION | | | INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1476 base pairs TYPE: uncleic acid | STRANDEDNESS: single TOPOLOGY: linear TAMBRIAND SOURCE. |

1056

255

1116

275

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216 ArgCysGluAspAlaTyrProArgGlnIleAspAspThrMetPheCysAlaGlyAspLys
                                     ArgProThrLysAspvalArgProIleAsnValSerSerHisCysProSerAlaGlyThr
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US-09-602-877A-94/C
Sequence 94, Application US/09602877A
Sequence 94, Application US/09602877A
Sequence 94, Application US/09602877A
SEQUENCE INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: W. Jiangchun
SAPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.446C5
CURRENT APPLICATION NUMBER: US/09/602,877A
CURRENT FILING DAME: 2000-06-22
NUMBER OF SEQ ID NOS: 107
SEQ ID NO 94
LIENGTH: 735
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Matches:
Conservative:
Mismatches:
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100.00%
100.00%
45.09%
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ORGANISM: Homo sapien
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Best Local Similarity:
Query Match:
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Pred. No.:
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Matches:
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Mismatches:
Indels:
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; OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-1
                                                                                                                                                                                                                                                                                          US-09-936-271B-14 (1-293) x US-09-280-116-1 (1-1504)
                                                               APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules 1
FILE REFRENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: Patentin Ver. 2.0
                          US-09-280-116-1
Sequence 1, Application US/09280116A
Patent No. 6331427
GENERAL INFORMATION:
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93.77%
91.80%
87.25%
                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens.
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Best Local Similarity:
Query Match:
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59 ArgSerAspAspSerSerArgIleIleAsnGlySerAspCys---AspMetHisThr 77
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                                                  161 ArgArgIleArgProThrLysAspValArgProIleAsnValSerSerHisCysProSer
                                                                        GAATCCGTGTCCGAGTCTGACACCATCCGGAGCATCAGCATTGCTTCGCAGTGCCCTACC
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                                                                                                                                                                                                                                                                                                                                                                                                              260 SerTrpGlyAspTyrProCysAlaArgProAsnArgProGlyValTyrThrAsnLeuCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 LysPheThrLysTrpIleGlnGluThrIleGlnAlaAsn 292
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Darrow, Andrew
APPLICANT: Oi, Jenson
APPLICANT: Oi, Jenson
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT APPLICATION NUMBER: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlnTrpLeuLeuThrAlaAlaHisCysArgLysLysValPheArgValArgLeuGlyHis 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----AGCTGCAGCCAAATCATAAACGCGAGGACTGCAGCCCGCACTCGCAGCCCTGG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 CAGGCGCCACTGGTCATGGAA---AACGAATTGTTCTGCTCGGGCGTCCTGGTGCATCCG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TyrSerLeuSerProValTyrGluSerGlyGlnGlnMetPheGlnGlyValLysSerIle 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 CACAGTCTTGAGGCCGACCAAGAGCCAGGGAGCCAGATGGTGGAGGCCAGCCTCTCCGTA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 ProHisProGlyTyrSerHisProGlyHisSerAsnAspLeuMetLeuIleLysLeuAsn 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 ThrValProSerGlySerAsnGlnAspLeuGlyAlaGlyAlaGlyGluAspAlaArgSer 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AspAspSerSerArgIlelleAsnGlySerAspCysAspMetHisThrGlnProTrp 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MetAlaThrAlaArgProProTrpMetTrpValLeuCysAlaLeuIleThrAlaLeuLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 LeuGlyValThrGluHisValLeuAlaAsnAsnAspValSerCysAspHisProSerAsn 40
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                                                                                                                                                                                                                                                                                                                                                APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THEIR TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERBNGE: 210121.427059;
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 524
LENGTH: 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-936-271B-14 (1-293) x US-09-439-313-524 (1-765)
                               # TGGATCCAGGAAACCATCCAGGCCAACTCC 345
              293
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Matches:
              TrplleGlnGluThrileGlnAlaAsnSer
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                                                                                                                                                                     APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Reed, Steven G.
APPLICANT: Realos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
                                                                                                                   Sequence 524, Application US/09439313
Patent No. 6329505
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671.00
61.77%
45.73%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                        GENERAL INFORMATION:
                                                                                                  US-09-439-313-524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
             284
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EARLIER FILING DATE: 1997-12-18
EARLIER FILING DATE: 1997-12-18
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER PILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PAtentin Ver. 2.0
SEQ ID NO 247
LENGTH: 1146
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/049,373

R FILING DATE: 1997-06-06

R PILING DATE: 1997-06-06

R PILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/049,374
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R APPLICATION NUMBER: 60/048,897
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,898
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,992
                                                                                                    R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,884
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,894
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,971
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/048,900 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,901 FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/048,970 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/048,917
FILING DATE: 1997-06-06
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1997-06-06
APPLICATION UNDBER: 60/048,974
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,883
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,877
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                                                                                                                                                                                                                                 FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,964
FILING DATE: 1997-06-06
FILING DATE: 1997-06-06
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,893
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/048,915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/049,019
FILING DATE: 1997-06-06
               TILING DATE: 1997-06-06
PPLICATION NUMBER: 60/048,876
                                                                                  PPLICATION NUMBER: 60/048,895
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/048,899
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                                                             90-90-266
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BARLIER F
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436 ATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGCACCCCTCACC 495
142 GCCCCCTTTGATGATGATGATGGTGGTGTGTGTACAACTGTCTAGAAAAGCACTCC 201
                                                                                    98 ValHisProGlnTrpLeuLeuThrAlaAlaHisCysArgLysLysValPheArgValArg 117
                                                                                                                                                                                                                                      118 LeuGlyHisTyrSerLeuSerProValTyrGluSerGlyGlnGlnMetPheGlnGlyVal 137
                                                                                                                                                                                                                                                                                                                               LysSerIleProHisProGlyTyrSer------HisProGlyHisSerAsnAsp 153
                                                                                                                                                                                                                                                                                                                                                                     376 GAGTCCTTCCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAGACCACCGCAATGAC 435
                                                                                                                                                                                                                                                                                                                                                                                                                 LeuMetLeuIleLysLeuAsnArgArgIleArgProThrLysAspValArgProIleAsn 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 ValSerSerHisCysProSerAlaGlyThrLysCysLeuValSerGlyTrpGlyThrThr 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 LysSerProGlnValHisPheProLysValLeuGlnCysLeuAsnIleSerValLeuSer 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 GlnLysArgCysGluAspAlaTyrProArgGlnIleAspAspThrMetPheCysAlaGly 233
                                                             GlnProTrpGlnAlaAlaLeuLeuLeuArgProAsnGlnLeuTyrCysGlyAlaValLeu 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 GlySerLeuGlnGlyLeuValSerTrpGlyAspTyrProCysAlaArgProAsnArgPro
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TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 247, Application US/09205258 Patent No. 6525174 GENERAL INFORMATION:
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|CT 858
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NOVEL SERINE PROTEASE REACENTS
AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
OF THE PROSTATE
                                                                                                                                                 261 TrpGlyAspTyrProCysAlaArgProAsnArgProGlyValTyrThrAsnLeuCysLys
   222 ProArgGlnIleAspAspThrMetPheCysAlaGly---AspLysAlaGlyArgAspSer
                                                                                                                                                                                                              281 PheThrLysTrplleGlnGluThrIleGlnAlaAsn 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
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                                                                                                                                                                                                                                                                                       ; Sequence 7, Application US/08944483
; Patent No. 6232456
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWARF, KEWT D.
APPLICANT: STEWARF, STEVEN D.
TITLE OF INVENTION: NOVEL SERIN
TITLE OF INVENTION: AND METHODS
ITLE OF INVENTION: OF THE PROS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Abbott Laboratorie
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                     APPLICANT: COHEN, MAURICE
APPLICANT: COLEITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLASS, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1166 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               652.50
68.67%
50.64%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60064-3500
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                          US-08-944-483-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuArgProAsnGlnLeuTyrCysGlyAlaValLeuValHisProGlnTrpLeuLeuThr 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaAlaHisCysArgLysLysValPheArgValArgLeuGlyHisTyrSerLeuSerPro 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 ITCGAGAAGACGCGGCTACTCTGTGGGGCGACGCTCATCGCCCCCAGATGGCTCCTGACA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 GCAGCCCACTGCCTCAAGCCCCGCTACATAGTTCACCTGGGGCAGCACAACCTCCAGAAG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 GlyThrLysCysLeuValSerGlyTrpGlyThrThrLysSerProGlnValHisPhePro 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 LysValLeuGlnCysLeuAsnIleSerValLeuSerGlnLysArgCysGluAspAlaTyr 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---GAGGAGGCTGTGAGCAGACCCGGACAGCCACTGAGTCCTTCCCCACCCGGCTTC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 ArgIleArgProThrLysAspValArgProIleAsnValSerSerHisCysProSerAla 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 HisValLeuAlaAsnAsnAspValSerCysAspHisProSerAsnThrValProSerGly 45
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OTHER INFORMATION:
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US-08-790-137-2
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                                                                                                                          LeuLeuArgProAsnGlnLeuTyrCysGlyAlaValLeuValHisProGlnTrpLeuLeu 104
                                                                                                                                                                                  ThralaalaHisCysArgLysLysValPheArgValArgLeuGlyHisTyrSerLeuSer 124
                                                                                                                                                                                                                                                                                                                          394 TTCAACAACAGCCTCCCCAACAAGACCACCGCAATGACATCATGCTGGTGAAGATGGCA 453
                                                                                                                                          ACAGCAGCCCACTGCCTCAAGCCCCGCTACATAGTTCACCTGGGGCAGCACAACCTCCAG
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; Patent No. 5840871
; GENERAL INFORMATION:
    APPLICANT: HILIMAN, Jennifer L.
    TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCIATED
    TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCIATED
    TITLE OF INVENTION: KALLIKREIN
    NUMBER OF SEQUENCES:
    ADDRESSEE: Incyte Pharmaceuticals, Inc.
    STREET: 314 Porter Drive
                                         US-09-936-271B-14 (1-293) x US-08-944-483-7 (1-1166)
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MEDIUM TYPE: Diskette
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128 GluSerGlyGlnGlnMetPheGlnGlyValLysSerIleProHisProGlyTyrSer--- 146
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DOS
for Windows Version
                    SOFTWARE: FastSEQ for Windows Ver
CURREW APPLICATION DATA:
APPLICATION UNMER: US/08/790,137
FILING DATE: Filed Herewith
                                                                                                                                                                                                                   NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                          FILING DATE: ATTORNEY/AGENT INFORMATION:
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58.62%
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TYPE: nucleic acid
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                                                                                      FILING DATE: Filed He CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER:
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| 223 575 242 | | 755 Qy 85 I Db 221 C | Db 281 ACAGCAGCCCAC Qy 125 ProValTyrGlu Db 341 AAGGAGGAG Qy 145 TyrSer Db 398 TYCAACAACAG | Oy 161 ArgArgIleArg ::: | Qy 201 ProLysvalLeu 1 1 1 1 1 1 221 TyrProArgGln 1 1 Db 638 TACCCGGCAAC | Oy 240 SerCysGlnGly | 280 | RESULT 13 US-09-205-226-189 Sequence 189, Applicatio Patent No. 6525174 GENERAL INFORMATION: TITE OF INVENTION: CURRENT APPLICATION NUM CURRENT FILING DATE: 19 EARLIER FILING DATE: 19 |
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| Qy 204 LeuGlnCysLeuAsnIleSerValLeuSerGlnLysArgCysGluAspAlaTyrProArg Db 111::: | 243 636 263 | | RESULT 12 US-08-944-483-8 IS-2040ence 8, Application US/08944483 Patent No. 6232456 GENERAL INFORMATION: APPLICANT: COHEN, MAURICE APPLICANT: TRACEY I. APPLICANT: GRANADOS, EDWARD N. | APPLICANT: RLASS, MICHAEL R. APPLICANT: RUSSELL, JOHN C. APPLICANT: STEWART, KENT D. APPLICANT: STROUPE, STEVEN D. TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES INDUBER OF SEQUENCES: 76 | COUNTEX TE READLE FORM: | MEDIUM TYPE: DISKETCE COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/944,483 FILING DATE: CLASSIFICATION: 424 | PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE: ATTORNEY, AGENT INFORMATION: NAME: BECKET, Chervl I. | 32223. 3222. 33483. |

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------HisProGlyHisSerAsnAspLeuMetLeuIleLysLeuAsn 160
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scctccccaacaaaGaccaccacaarGacarCarGcrGcrGarGaAGArGGCA 457
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                                                                                                                                                                                                                       uSerGlyGlnGlnMetPheGlnGlyValLysSerIleProHisProGly 144
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07 Human Secreted Proteins
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1998-06-04
NUMBER: 60/048,885
1997-06-06
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PLICATION NUMBER: 60/049, 019
LING DATE: 1997-06-06
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LING DATE: 1997-06-06
PLICATION NUMBER: 60/048,877
                                                                                            LING DATE: 1997-06-06
PLICATION NUMBER: 60/048,896
LING DATE: 1997-06-06
                                                                                                                                                      PLICATION NUMBER: 60/049,020
LING DATE: 1997-06-06
                                                                                                                                                                                                                                    PLICATION NUMBER: 60/048,895
LING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/048,893
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,915
FILING DATE: 1997-06-06
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PLICATION NUMBER: 60/048,972
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APPLICATION NUMBER: 60/049,373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,974
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APPLICATION NUMBER: 60/048,962
FILING DATE: 1997-06-06
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LING DATE: 1997-12-18
APPLICATION NUMBER: 60/049,375
                                    PLICATION NUMBER: 60/048,881
LING DATE: 1997-06-06
                                                                              APPLICATION NUMBER: 60/048,880
                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,964
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/048,882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/048,899
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                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/048,894
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Application US/09025059

Sequence 2, Ap Patent No. 607 RESULT 14 US-09-025-059-2

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161 ArgArgIleArgProThrLysAspValArgProIleAsnValSerSerHisCysProSer 180
                                                                                           AlaglyThrLysCysLeuValSerGlyTrpGlyThrThrLysSerProGlnValHisPhe 200
                                                                                                                                                                                                           695 CCTCACACCTTGCGATGCGCCAACATCACCATGATGAGCACCAGAAGTGTGAGAACGCC 754
                                                                                                                                                                                                                                                                            260 SerTrpGlyAspTyrProCysAlaArgProAsnArgProGlyValTyrThrAsnLeuCys 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             935 AAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purvi
OF INVENTION: HUMAN PROTEASE MOLECULES
OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
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REFERENCE/DOCKET NUMBER: PF-0458 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: <Unknown>FILING DATE: <Unknown>
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Hillman, Jennifer
Yue, Henry
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STRANDEDNESS: single
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                  APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARR: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/025,059
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Matches:
                                                                                                                                  3: Incyte Pharmaceuticals, Inc 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0481 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                     ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1314 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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50.64%
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APPLICATION NUMBER:
FILING DATE:
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CITY: Palo Alto
STATE: CA
GENERAL INFORMATION:
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Best Local Similarity:
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                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 LysSerProGlnValHisPheProLysValLeuGlnCysLeuAsnIleSerValLeuSer 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ValLysSerIleProHisProGlyTyrSerHis-----ProGlyHisSerAsnAsp 153
                                                                                                                                                                                                                                                                                                        57 AspAlaArgSerAspAspSerSerSerArgIleIleAsnGlySerAspCysAspMetHis 76
                                                                                                                                                                                                                           17 ThralaLeuLeuLeuGlyValThrGluHisValLeuAlaAsnAsnAspValSerCysAsp 36
                                                                                                                                                                                                                                                                  37 HisProSerAsnThrValProSerGlySerAsnGlnAspLeuGlyAlaGlyAlaGlyGlu 56
                                                                                                                                                                                   -----ProTrpMetTrpValLeuCysAlaLeuIle 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlnLysArgCysGluAspAlaTyrProArgGlnIleAspAspThrMetPheCysAlaGly
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126
43
80
7
                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                               US-09-936-271B-14 (1-293) x US-09-008-271A-19 (1-994)
TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBERRY: COLNNOT27
: CLONE: 1798496
: SEQUENCE DESCRIPTION: SEQ ID NO: 19
US-09-008-271A-19
                                                                                                                                            Gaps:
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639.50
57.09%
42.57%
                                                                                                             Percent Similarity:
Best Local Similarity:
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